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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification<sup>6</sup> :</b> <b>C12N 5/14, 7/04</b>	<b>A1</b>	<b>(11) International Publication Number:</b> <b>WO 97/39110</b> <b>(43) International Publication Date:</b> 23 October 1997 (23.10.97)
<b>(21) International Application Number:</b> PCT/US97/06300 <b>(22) International Filing Date:</b> 15 April 1997 (15.04.97) <b>(30) Priority Data:</b> 60/015,517      16 April 1996 (16.04.96)      US <b>(71) Applicants:</b> SEMINIS VEGETABLE SEEDS, INC. [US/US]; 1905 Lirio Street, Saticoy, CA 93007 (US). WISCONSIN ALUMNI RESEARCH FOUNDATION [US/US]; P.O. Box 7365, Madison, WI 53707-7365 (US). <b>(72) Inventors:</b> STOUT, John, T.; 2900 Hunter's Hill, Kalamazoo, MI 49004 (US). LUU, Hang, T.; 6235 San Gabriel Drive, Kalamazoo, MI 49009 (US). HANSON, Steven, F.; 1609 Jefferson Street, Madison, WI 53711 (US). MAXWELL, Douglas, P.; 7711 Midtown Road, Verona, WI 53593 (US). AHLQUIST, Paul, G.; 3106 Bluff Street, Madison, WI 53705 (US). <b>(74) Agents:</b> MUELLER, Lisa, V. et al.; Dressler, Rockey, Mil- namow & Katz, Suite 4700, Two Prudential Plaza, 180 North Stetson Avenue, Chicago, IL 60601 (US).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> TRANSGENIC PLANTS EXPRESSING GEMINIVIRUS GENES  <b>(57) Abstract</b>  The invention involves production of transgenic plants containing DNA encoding AC1/C1 wildtype and mutant sequences that negatively interfere in trans with geminiviral replication during infection. The transgenic plants produced by the invention are resistant to viral infection.		

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TITLETRANSGENIC PLANTS EXPRESSING GEMINIVIRUS GENES

5

Description of Invention

A variety of geminivirus genes and mutant derivatives were generated and transferred to plant cells.

- 10 Transgenic plants containing these genes were produced. Transgenic plants containing trans-dominant mutations developed resistance to geminivirus infection.

BACKGROUND

15

Geminiviruses present the most serious disease problem in many vegetable crops in tropical and subtropical regions. For example, major epidemics of geminivirus infections of beans and tomatoes have occurred in

- 20 Florida, the Caribbean Basin, Mexico, and Central America. In the past, traditional breeding methods failed to produce cultivars with significant levels of resistance to geminiviruses. An alternative approach lies in producing virus-resistant transgenic plants
- 25 according to the present invention.

The geminivirus group are single stranded DNA viruses that infect both monocotyledonous (monocot) and dicotyledonous (dicot) plants. A common feature among all gemini viruses is the mode of genomic replication, which involves a rolling circle mechanism.

Tomato mottle virus (ToMoV) is one example of a geminivirus. It has a two component (bipartite) genome, an ability to infect dicot plants and is transmitted by whitefly. The DNA of its two genomic components, DNA-A and DNA-B, has previously been cloned and sequenced. Isolated clones of DNA-A and DNA-B of ToMoV are themselves infectious when mechanically inoculated into tomato and *N. benthamiana*, or when delivered to either host by agroinoculation. An invariant geminiviral DNA sequence required for replication is present in an intergenic, common region (CR) in each genomic component.

The ToMoV DNA-A genomic component has four ORF, one of which, AC1, must be expressed for efficient replication of both A and B components. The AC1 ORF encodes a protein having several functional activities: a DNA binding site specific to the DNA-A CR; a DNA nicking activity; and a NTP binding activity. The DNA binding region mediates an initiator protein function during rolling circle replication.

AC3 protein is a second ToMoV-coded function involved in DNA replication and production of single-stranded circular DNA.

Tomato yellow leaf curl virus (TYLCV) is another example of a geminivirus. TYLCV has a monopartite genome organization, infects monocot plants, and is leaf-hopper transmitted. The TYLCV C1 protein is required for replication, encoded by the C1 ORF.

Being DNA viruses, geminiviruses offer advantages for antiviral strategies. Several geminiviruses have been cloned and sequenced. Transgenic plants having mutant viral genes can be produced, e.g., by introducing  
5 expression cassettes comprising mutated virus genes directly into plants with a particle gun, or into plant suspension cells or protoplasts by electroporation, or by Agrobacterium transfection.

10                                    Summary Of The Invention

The invention involves production of transgenic plants containing DNA encoding AC1/C1 wildtype and mutant sequences that negatively interfere in trans with  
15 geminiviral replication during infection. The resulting transgenic plants are resistant to viral infection.

Description of the Figure

Fig. 1 shows the results of a transient assay for  
20 trans-dominance done with BGMV-GA in NT-1 cells.

Detailed Description Of The Invention

A. Production of infectious clones

25 Infectious clones of geminiviruses are produced by methods known to the skilled worker. Geminivirus DNA is extracted from tissue as follows. Young tissue is collected from infected plants, frozen in liquid nitrogen and ground in a mortar in the presence of  
30 extraction buffer (10 mM Tris-Cl, pH 7.5, 10 mM EDTA, and 1% SDS, 1:4 wt/vol ratio) and centrifuged for about 10<sup>5</sup> g minutes. The supernatant is adjusted to about 1 M NaCl and stored at about 4°C for about 12 hr, then centrifuged for about 10<sup>7</sup> g minutes. After phenol  
35 extraction, the solution is adjusted to 0.3 M sodium acetate, and the DNA is precipitated in alcohol. Viral nucleic acids are isolated by agarose gel electrophoresis.

These viral nucleic acid fractions are digested with restriction enzymes and isolated by agarose gel electrophoresis. The DNA is cloned in a suitable cloning vector, e.g., pBluescript KS+, and its identity  
5 is confirmed by sequencing.

Full-length clones of the geminivirus genome are constructed, e.g., by a PCR-based cloning strategy. Primers are synthesized that will amplify the entire  
10 ORF plus about ten nucleotides on each side of the ORF. The primers should include mismatched bases to create restriction sites before and after the C1 or AC1 ORF which will allow convenient cloning without altering initiation and termination codons of C1 or AC1 ORFs.

15  
Primer 1 is complementary to and anneals with the viral sense strand of the geminiviral genome. The 5' end of the primer is located 40-50 base pairs 3' of the translation start, and the 3' end is located 10-20 base  
20 pairs 3' of the translation start site. Translation start is defined by CAT on the viral sense strand; AC1 or C1 ORFs are located on the complementary strand of the viral genome and sequence coordinates are given for the viral sense polarity strands.

25  
Primer 2 is complementary to and anneals with the strand (complementary sense polarity) of the geminiviral genome. The 5' end of the primer is located 40-50 base pairs 3' of the AC1 or C1  
30 termination condon, and the 3' end of the primer is located 10-20 base pairs 3' of the translation stop as determined on the complementary sense polarity strand.

The primers are used in a PCR reaction to amplify the  
35 C1 or AC1 ORF from cloned viral DNA or purified geminivirus DNA. The amplified DNA is digested with appropriate restriction enzymes to cut sites engineered in the ends of the PCR fragment and the resulting fragment is cloned into a suitable vector. C1- or AC1-

containing clones are identified and sequenced to confirm the presence and integrity of the cloned C1 or AC1 ORF.

- 5 The sequence of the AC1/C1 ORF is used for designing the primers for amplification of the PCR fragment of AC1/C1 ORF. For example, these primers are designed so that this ORF is cloned into the BamHI and HindIII sites of pBluescript KS+. The BamHI site is located
- 10 at the 5' end of the complementary sense primer, which amplifies the amino terminal end of the ORF. A HindIII site is located at the 5' end of the viral sense primer which anneals to the carboxy end of the ORF.
- 15 Infectious clones preferably are selected. The infectivity of the clones are determined by construction of *Agrobacterium* having greater-than-full-length viral genes with at least two common regions of DNA-A and DNA-B. Infectivity is determined by
- 20 microparticle inoculation. Seeds are germinated on moist filter paper to produce 1-3 cm long radicles of a host, and this tissue is bombarded by DNA-coated particles with a particle gun. Inoculated plants are placed in a growth chamber at about 26°C with about 14
- 25 hour photoperiods. Infectivity is confirmed by PCR with primers specific for geminiviruses or Southern blot analysis. For example, 1.3-kb PCR products are expected when primers PAL1v1978 and PAV1c715 are used.
- 30 Cloned viral DNA is digested with restriction enzymes and analyzed on agarose gels to produce a unique 2.5 to 2.7-kb fragment. The DNA bands are removed from the gel and cloned into an appropriate vector. For monopartite geminiviruses, the insert preferably
- 35 includes the entire genome. For bipartite geminiviruses, entire inserts of both genomic components are preferable. The single insert of the monopartite geminivirus or both cloned components of bipartite geminiviruses are introduced into a host



plant and tested for infectivity by biolistic delivery or agroinoculation.

The cloned C1 (monopartite viruses) or AC1 (bipartite viruses) ORF are isolated by selecting for the following characteristics:

- 10           A.    The AC1 or C1 ORF encodes a protein product of about 42 Kd.
- 15           B.    The nucleotide sequence of the C1 or AC1 ORF is at least 60% homologous to the AC1 ORF of a previously identified geminiviruses (e.g., BDMV, ToMoV, or TYLCV). The deduced amino acid sequence of the ORF will contain several characteristic sequences which are similar in sequence and relative position within the ORF i.e., motifs within the C1 or AC1 sequences.

20           B.    Introducing Mutations

      Mutations are introduced by site-directed mutagenesis of cloned C1 or AC1 ORF by methods known in the art, e.g., using the method of Kunkel et al. (Recombinant DNA Methodology, 1989, pp. 587-601) (herein, "Kunkel mutagenesis").

      In particular, mutations are introduced into amino acid sequence motifs in C1 or AC1 ORF that are highly conserved among all gemini viruses. Four motifs are preferred in the DNA-nicking domain of the protein. These include (capital letters denote high conservation of amino acid, lower case denotes some conservation, and "x" denotes a variable position in the motif):

- (1)   FLTYpxC
- 35          (2)   HlHvliQ
- (3)   vKxYxdKd; and

(4) FHPNIQxak.

Additionally two motifs are preferred in the NTP-binding domain of the protein. These include:

- 5           (5) EGx<sub>2</sub>RTGKt; and  
            (6) NviDDi.

The individual codons specifying the most highly conserved amino acids within these motifs are  
10   mututated. For example, one or more of the following mutations introduced to the C1 or AC1 ORF:

- (1) vKxYxdKd to (a) vKxFxdKd;  
                                (b) vKxAxdKd;  
                                (c) vKxYxdRd;  
15           (2) EGx<sub>2</sub>RTGKt to (a) EGx<sub>2</sub>RTGHt;  
                                (b) EGx<sub>2</sub>RTGAt;  
                                (c) RGx<sub>2</sub>RTGKht;  
            (3) NviDDi to (a) NviRDi;  
                                (b) NviKDi; or  
20                               (c) NviDYi,

(herein mutations 1(a), 1(b), 1(c), 2(a), 2(b), 2(c), and 3(a), 3(b), 3(c), respectively). Acidic or basic amino acids are changed to the opposite charge, to  
25   alanine (alanine scanning) or to other neutral amino acids. Combinations of mutants are also made. For example, a single C1 or AC1 ORF containing codon changes corresponding to vKxFxdKd and EGx<sub>2</sub>RTGHt (double mutations 1(a) and 2(a), above) are constructed and

tested. Other mutants in motifs within AC1/C1 are possible and are used. The presence of the codon change is confirmed by DNA sequencing.

*Agrobacterium*-mediated transfer of the plant

5 expressible mutated AC1/C1 ORF is done using procedures known to those skilled in the art.

If an infectious clone of the geminivirus is available, effects of mutations on replication can be tested. The  
10 mutation is introduced into the C1 or AC1 ORF of an infectious clone. Mutant DNA is transferred to plant cells. Replication of wild type viruses is tested for infection as a positive control. Mutations which create transdominant molecules generally abolish  
15 replication when engineered into infectious clones. A number of mutations which change codons for conserved amino acids within these motifs will be lethal and potentially transdominant. Other mutations in C1 or AC1 which abolish replication should also be considered  
20 potentially transdominant. Any non-functional C1 or AC1 molecule has the potential to be transdominant.

Mutated C1 or AC1 ORFs are installed into a suitable plant transformation vector in the sense orientation  
25 and under the control of a strong constitutive promoter sequence and suitable terminator for high level expression in the target plant species. This step is performed for each of the C1/AC1 mutants created.

C. Assays

- A transient assay is useful to screen candidate constructs for transdominant interference activity. This is done by first coinoculating protoplasts or a
- 5 plant cell suspension culture with the infectious geminivirus clone and a plasmid containing mutant C1 or AC1 ORF under control of a strong constitutive plant promoter. Control treatments are inoculated with an infectious clone. Total DNA is harvested from
- 10 inoculated cells, and is assayed for viral replication. Transdominant C1 or AC1 mutants are identified as those which suppress geminiviral replication relative to control treatments after coinoculation.
- 15 In vitro assays for transdominance correlate lethal mutations and transdominant activity in transient assays. This is exemplified in a BGMV-GA model system. These results are readily applicable to produce a transdominant C1 or AC1 ORFs from other geminiviruses.
- 20 Transgenic plants resistant to ToMoV were created by transforming them with an AC1 ORF derived from ToMoV and engineered to contain similar mutations.

Expression cassettes constructed above are installed

25 into binary plasmids and transformed into *Agrobacterium* strains for plant transformation protocols. Plants are transformed by methods tailored to the specific variety or line.

Transgenic status of  $R_0$  and later generation plants and their segregating progeny is verified by routine methods, including: ELISA assays for NPTII protein detection; DNA assays such as PCR amplification with the AC1/C1 primers of plants and Southern blot hybridization for detection of transgenes using AC1/C1 as viral probes; and Southern blot hybridization to detect ACI or CI transgenes. Demonstration that  $R_1$  plants transformed with geminivirus gene constructions express NPTII protein is done by ELISA. Protein in leaf tissue samples taken from  $R_1$  transgenic plant seedlings is extracted and analyzed for NPTII protein by ELISA.

Geminivirus transgene expression is also measured by Northern blot analysis. Transgene expression in a number of  $R_0$  and  $R_1$  plants was done by Northern blot hybridization. Total RNA extracted from leaves of transgenic plants is separated by agarose gel electrophoresis. After electrophoresis, RNA is pressure blotted onto membrane. Membranes are hybridized with radiolabeled probes, washed, and autoradiographed.

D. Identification of gemini-resistant transgenic plants

Geminivirus-resistant transgenic plants are identified by challenging transgenic plants and progeny.  $R_1$  plants from self pollinated  $R_0$  primary regenerants are

agroinoculated about 3 weeks after sowing. Alternative methods include biolistic inoculation, sap transmission from infected tissue (if the isolate is mechanically transmissible), insect transmission, or grafting. For  
5 bipartite geminiviruses, agroinoculation preferably involves delivery of greater-than-full-length (i.e., at least 2 common regions) DNA-A and DNA-B components into the seedlings using *Agrobacterium* strains, e.g., containing a binary vector having in its T-DNA a  
10 partial or full tandem duplication of infectious geminivirus DNA. Geminivirus-resistant plants are incorporated into traditional breeding programs to develop elite breeding lines that include the resistance-conferring transgene. These changes produce  
15 C1 or AC1 molecules when made alone or in combination with a mutant.

Plants showing the highest steady state levels of transgene RNA are challenged by *Agrobacterium*-mediated inoculation. Resistance is  
20 determined by lack or delay of symptom expression and low levels of viral DNA in plants as determined by squash blot hybridization tests with viral probes (Gilbertson et al., 1991. Plant Disease 75:336-342.). Resistance is also determined by inoculation with  
25 viruliferous *Bemisia tabaci* as described. It is expected that plants with low levels of mRNA accumulation for the mutated AC1/C1 ORF have symptoms and those with high levels have no symptoms.

Since the AC1/C1 proteins have domains required for DNA-nicking and NTP-binding that are conserved among all geminiviruses, an antiviral strategy involving mutated AC1/C1 protein is applicable to

5 plant-geminivirus systems in general.

Other viruses include:

	Virus	Genes/Regions	SEQ ID NO.
10	TGV-GA1	AC1 ORF DNA-A (complementary seq)	57
	TGV-GA1	Common & Intergenic Region (viral)	58
	TLCV-IND	Full Length Sequence (stemloop begin)	59
	"Chino"	Partial AC1, Common region, AV1	60
	PHV	AC1, Common region, Intergenic, AV1	61
15	PHV	BV1 ORF	62
	PHV	BC1, Hypervar., Common, & Interg. Reg	63

The following examples are offered by way of illustration and not by way of limitation.

20

#### EXAMPLE 1. Gene Expression Vectors

All *E. coli* culture and plasmid DNA isolation methods were carried out according to standard methods.

25 Restriction digestions, filling in of 5' end overhangs, calf intestinal alkaline phosphatase treatments of DNA and ligation of DNA fragments and gel electrophoretic separation of DNA fragments and their isolation from gels were done according to manufacturers'

recommendations and methods. *Agrobacterium* large plasmid DNA was isolated. *Agrobacterium* transformation and culture is performed according to general methods known to those skilled in the art.

5

Tables 1A and 1B list geminiviral transcribed sequences, expression vectors, binary plasmids, and *Agrobacterium* strains described in the Examples.



Tabl 1A. Constructs used to Creat Transgenic Plants

	Transcribed Seq. (open reading frame or antisense seq.)	Expression Vector Used	Binary Vector Used	<i>Agrobacterium</i> <i>tumefaciens</i> designation
5	ToMoV-AC1 <sub>as</sub>	pRT101e	pJTS246Δ	RTAC
	ToMoV-AC1	pRT101e	pJTS246Δ	RTSC
	ToMoV-AC1 <sub>as</sub>	DH51	pJTS235	DHAC
	ToMoV-AC1	DH51	pJTS235	DHSC
10	ToMoV-AC1-AC2-AC3 <sub>as</sub>	pRT101e	pJTS246Δ	RT3AA
	ToMoV-AC1 <sub>as</sub>	pRT101e	pJTS246Δ	RTFS
	ToMoV-AC1	pLAT	pJTS246Δ	LASD, LASU
	ToMoV-AC1dlm	pRT101e	pJTS246Δ	MEU
	ToMoV-AC1dlm	pRT101e	pJTS246Δ	MEU2
15	ToMoV-AC1dlm1	pRT101e	pJTS246Δ	MUA
	ToMoV-AC1dlm23	pRT101e	pJTS246Δ	MUB
	ToMoV-AC1	pΔ1CO35	pJTS246Δ	COALS
	ToMoV-AC1dlm	pΔ1CO35	pJTS246Δ	COCLM
	ToMoV-AC1dlm1	pRTIN	pJTS246Δ	MUADN
20	ToMoV-AC1dlm23	pRTIN	pJTS246Δ	MUBIN
	TYLCV-C1 <sub>as</sub>	pRT101e	pJTS246Δ	LCA
	TYLCV-ΔC2 <sub>as</sub> TYLCV-C1 <sub>as</sub>	pRT101e	pJTS246Δ	LCR <sup>+</sup>
	TYLCV-V1 <sub>as</sub>	pRT101e	pJTS246Δ	LCR <sup>+</sup>
25	TYLCV-C1-ΔC2-ΔC3 <sub>as</sub>	pRT101e	pJTS246Δ	RT3CA
	TYLCV-C1-ΔC2-ΔC3 <sub>as</sub>	pΔ1CO35	pJTS246Δ	CO3CA
	TYLCV-C104	eP <sub>ms</sub> -T <sub>ms</sub>	pGA482Δ + HYG <sup>R</sup>	C104
	TYLCV-C225	eP <sub>ms</sub> -T <sub>ms</sub>	pGA482Δ + HYG <sup>R</sup>	C225
	TYLCV-C259	eP <sub>ms</sub> -T <sub>ms</sub>	pGA482Δ + HYG <sup>R</sup>	C259
30	TYLCV-C1-ΔC2-ΔC3	pRT101e	pJTS246Δ	RT3CS

Table 1B. Constructs for *Agrobacterium* Inoculation

	Geminivirus strain and Sequence	Binary Vector Used	<i>Agrobacterium</i> Designation
35	ToMoV-A dimer	pJTS222	A.t. ToMoV-A
	ToMoV-B 1.67mer	pJTS222	A.t. ToMoV-B
40	TYLCV-EG dimer	pJTS222	A.t. TYLC-EG

**Example 1.1 Synthesis of expression vector pRT101e**

The pRT101e expression vector listed in Table 1A was made by removing a 325-bp HindIII-EcoRV fragment from pUC8-CaMVCAT (Pharmacia) and inserting it into HincII-HindIII-digested pRT101 (Dr. Topfer, Max Planck-Institut fur Zuchtungsforschung, 5000 Koln 30, Germany), thereby adding a segment of the 35S promoter containing the upstream enhancer (Kay et al., Science, 1987, 236:1299-1302) to the 5' end of the 35S promoter sequence of pRT101.

**Example 1.2 Expression vector pDH51**

The pDH51 expression vector of Table 1A (T. Hohn, Friedrich Miescher Institute, P.O. Box 2543, CH-4002, Basel, Switzerland) is comprised of a CaMV 35S promoter-35S terminator expression cassette.

**Example 1.3 Synthesis of expression vector pA1C035**

The pA1C035 expression vector of Table 1A was derived from pCO1bam (Dr. Neil Olszewski, University of Minnesota-Twin Cities, College of Biological Sciences). The 1.0-kb EcoRI-SalI fragment of pCO1bam, containing the promoter controlling expression of the commelina yellow mottle virus (CoYMV) transcript (Medberry et al., Plant Cell, 1992, 4:185-92), was inserted into EcoRI-SalI-digested pSL1180 (Pharmacia). A 1.1-kb EcoRI-DraI fragment of the resulting construct was inserted into EcoRI-HincII-digested pRT101, thereby replacing the CaMV 35S promoter of pRT101 with the CoYMV promoter. Some restriction sites, including BamHI and BglII, were removed by partially digesting this plasmid with HindIII and recircularizing it with T4 DNA ligase to produce pA1C035.

**Example 1.4 Synthesis of expression vector pRTIN**

The pRTIN expression vector of Table 1A is a derivative of pRT101e and pCOIN, in which the 35S terminator of pRT101e was replaced with the protease inhibitor gene terminator/polyadenylation site ( $T_{NH}$ ) of pCOIN. To

produce pCOIN, the 760-bp HindIII-XbaI fragment of pTPI-1 (Dr. C. Ryan, Washington State University, Pullman, WA) containing  $T_{NH}$  was inserted into HindIII-XbaI-digested Bluescript II KS+ (Stratagene). The 770-  
 5 bp XbaI-KpnI fragment of the resulting construct was inserted into XbaI-KpnI-digested pUC19. The 800-bp PstI-KpnI terminator fragment of the resulting plasmid was ligated with the KpnI-PstI fragment of pAlCO35 to produce pCOIN. The 805-bp SphI-SspI fragment of pCOIN  
 10 was inserted into SphI-SmaI-digested pRT101e, thereby replacing the 35S terminator of pRT101e with  $T_{NH}$ . The resulting plasmid was further modified by inserting into a EcoRI site a DNA fragment with EcoRI ends and internal restriction sites including BamHI to produce  
 15 pRTIN.

#### Example 1.5 Synthesis of expression vector $eP_{mas}-T_{phas}$

The expression vector  $eP_{mas}-T_{phas}$  of Table 1A was assembled  
 20 by combining an octopine synthase upstream activating sequence (ocs UAS) and a mannopine synthase promoter (*mas2'*).

The ocs UAS was excised from pAL1050 (Dr. Paul J.J. Hooykaas, State Univ. of Leiden, 2333 AL Leiden, The Netherlands), which was isolated from *Agrobacterium tumefaciens* strain LBA4404 (Dr. P.J.J. Hooykaas). A 2.8-kb EcoRI fragment of pAL1050, containing nt 13362-16202 of ocs UAS was inserted into the EcoRI site of  
 30 pSL1180 (Pharmacia). A 311-bp SacI-BamHI fragment of the resulting plasmid, containing nt 13774-14085 of the ocs UAS, was ligated into SacI-BamHI-digested pBluescript II KS+. A 285-bp XhoI-MfeI fragment containing the ocs UAS was ligated with the EcoRI-XhoI  
 35 fragment of pBluescript II KS+ with ocs UAS to produce a plasmids having tandemly repeated ocs UAS element structure. A EcoRI-XhoI fragment of the recombinant plasmid was ligated with another MfeI-XhoI fragment to

produce a recombinant plasmid, pBluescript+UAS<sup>3</sup>, having three tandemly repeated ocs UAS elements.

The *mas2'* promoter element was isolated as follows.

- 5 Plasmid pE93 (Dr. Stan Gelvin, Purdue University) is derived from pRK290 (Ditta et al., 1980). EcoRI fragment #13 of pE93 contains nt 16202-21634 of the octopine Ti plasmid, and lacks an internal ClaI fragment at nt 8672-20128 (Eco13ΔCla). A 4-kb EcoRI-
- 10 XhoI fragment was ligated with the SalI-EcoRI fragment of pBR322, to produce pJTS213. This plasmid was introduced into *E. coli* GM119 (Dr. Gurnam Gill, Pharmacia & Upjohn, Kalamazoo, MI), which is deficient in DNA adenine methylation. Thus, normally
- 15 undigestible ClaI site beginning at nt 20128 in Eco13ΔCla is cleavable by ClaI. A 951-bp ClaI-NcoI fragment of pJTS213 containing nt 21079-20128 was isolated and ligated with the ClaI-NcoI fragment of pSL1180 to produce pSL1180+P<sub>mas</sub>.

20

- A ocs UAS-enhanced mannopine synthase promoter cassette (Ep<sub>mas</sub>) was assembled as follows. A 365-bp ClaI-FspI *mas2'* fragment from pSL1180+P<sub>mas</sub> was ligated with the ClaI-EcoRV fragment of pBluescript + UAS<sup>3</sup>. Clones in
- 25 which the *mas2'* was inserted downstream of the ocs UAS repeat were identified by restriction digestion. To facilitate the addition of the phaseolin transcription terminator, a 250-bp multiple cloning site (mcs) XhoI-SalI fragment from pSL1180 was ligated into the XhoI-
  - 30 digested recombinant plasmid. Two plasmids, pBluescript+UAS<sup>3</sup>+P<sub>mas</sub>+mcs (orientations I and II), containing a construct with the mcs inserted in the two possible orientations were isolated.

- 35 The phaseolin terminator was added to pBluescript+UAS<sup>3</sup>+P<sub>mas</sub>+mcs, completing the assembly of Ep<sub>mas</sub>-mcs-T<sub>phas</sub>, as follows. A 1.1-kb PstI-EcoRI fragment of pUC19-*hph*-T<sub>phas</sub> (described below in the assembly of pGA482Δ+HYG<sup>R</sup>), which contains the phaseolin

transcription terminator ( $T_{phas}$ ), was ligated with PstI-EcoRI-digested pBluescript II KS+. A 1.2-kb SacII-ClaI fragment of the resulting plasmid was ligated with the SacII-ClaI fragment of pBluescript+UAS<sup>3</sup>+P<sub>mas</sub>+mcs  
5 (orientation I) to produce a plasmid having the eP<sub>mas</sub>-T<sub>phas</sub> insert.

#### Example 1.6 Synthesis of expression vector pLAT

The expression vector pLAT of Table 1A was produced as  
10 follows. The promoter of the LAT52 gene (Twell et al., Development, 1990, 109:705-13) was used to construct an AC1 gene construct in sense orientation that does not express in vegetative tissue. A 600-bp NcoI-SalI fragment of pLAT52-7a (Dr. S. McCormick, Plant Gene  
15 Expression Center, USDA ARS, Albany, CA), which contains the LAT52 promoter, was ligated with NcoI-SalI-digested pSL1180 to produce pLAT.

#### Example 2.1 Synthesis of binary vector pJTS246A

20 The binary vector pJTS246A of Table 1A was produced as as a derivative of pGA482 (Dr. G. An, Washington State University, Pullman, WN), by replacing the nopaline synthase controlled NPTII sequence with a CaMV 35S promoter-NPTII-phaseolin terminator selectable marker.  
25 The selectable marker was situated at the left T-DNA border to insure that the passenger gene, inserted at the right T-DNA border, would be transferred into the plant cell.

30 A BamHI fragment of pUC8-CaMVCAT was ligated with a 2.2-kb BamHI fragment of pDOB513ro4.6K (J.L. Slightom, Pharmacia & Upjohn), containing the NPTII coding region and octopine Ti plasmid T-DNA ORF No. 26 transcription terminator, to produce pJTS228. The pJTS228 construct  
35 has the 2.2-kb fragment, inserted as a transcription fusion unit immediately downstream of the CaMV 35S promoter of pUC8-CaMVCAT. Most of the CAT gene of pUC8-CaMVCAT was deleted from pJTS228 by digesting with EcoRI to produce pJTS228A. A 4.0-kb BamHI-NcoI

- fragment from pJTS228 was ligated with a 1.55kb BamHI-NcoI fragment from pkanPhas (J.L. SLightom, Pharmacia & Upjohn) containing the NPTII coding sequences 5' distal to the NcoI site and the phaseolin terminator. A
- 5 resulting plasmid, in which the T-DNA transcription terminator fused to the NPTII ORF was replaced with the phaseolin storage protein terminator from *Phaseolus vulgaris*, was designated pJTS233.
- 10 pJTS233 was digested with HindIII and flush ended. A 2.8-kb EcoRI fragment containing the 35S promoter, NPTII coding region and phaseolin terminator was isolated and ligated in a 3-part reaction with SmaI-BamHI fragment of pUC9 and an 8.0-kb BamHI-EcoRI
- 15 fragment of pGA482 containing the broad host range replicon, left and right nopaline Ti T-DNA borders and nopaline synthase promoter. The desired construct, pJTS246, was cloned and isolated. pJTS246 was modified to eliminate the ampicillin drug resistance contributed
- 20 by pUC9. The plasmid was digested with ScaI and HindIII, and treated with HindIII linkers followed by HindIII digestion. The resulting plasmid, pJTS246Δ, had 1730-bp of pUC sequence deleted from pJTS246.
- 25       **Example 2.2 Synthesis of binary vector pJTL222**  
pJTS222 is pGA492 (Dr. G. An) in which a 2.2-kb BamHI-HindIII fragment replaced by the 430 bp BamHI-HindIII fragment of pUC8-CamVCAT containing the CaMV 35S promoter.
- 30       **Example 2.3 Synthesis of binary vector pJTS235**  
pJTS235 was a binary plasmid derived from pGA492 in which the NPTII coding sequence and its transcription terminator were removed and replaced with a CaMV 35S
- 35 promoter-NPTII coding sequence-phaseolin terminator selectable marker. pJTS235 was constructed by ligating a 2.1-kb BamHI fragment of pJTS233 containing the NPTII coding sequence and phaseolin terminator into the BamHI fragment of pJTS222. The resulting plasmid, pJTS235

had the NPTII structural gene under the control of 35S promoter.

#### Example 2.4 Synthesis of binary vector pJTS250

5 pJTS250 was assembled as follows. A 353-bp PstI-BamHI fragment of pLG90 (provided by Dr. L. Gritz, Biogen, S.A., 46 Route des Acacias, Geneva, Switzerland), which includes the entire hygromycin phosphotransferase gene (hph) coding region from the ATG translation start  
10 codon to 15 bp distal to the translation terminator, was ligated with the PstI-BamHI digest of pUC9 to produce pUC9+hph-a. Another aliquot of AvaI-digested pLG90 with AvaI flush ended. The 670-bp PstI fragment was cloned into the SmaI-PstI fragment of pUC9 to  
15 produce pUC9+hph-b, creating a 670-bp fragment PstI-EcoRI fragment. A 1.18-kb NaeI-BamHI fragment containing the phaseolin terminator (J.L. Slightom) was cloned into the BamHI-SmaI fragment of pUC9 to create pUC9+T<sub>phas</sub>. The above three fragments (353-, 670- and  
20 1180-bp) were ligated with the BamHI digest of pJTS222. The resulting binary plasmid, pJTS250, was produced comprised of a P<sub>35S</sub>-hph-T<sub>phas</sub> plant selectable marker, and the capability to transform plant tissue to hygromycin resistance via *Agrobacterium*-mediated gene transfer.

25

#### Example 2.5 Synthesis of binary vector pGA482A+HYG<sup>R</sup>

pGA482A+HYG<sup>R</sup> was produced from the following plasmids: pGA470 (Dr. G. An); pJTS262, including the entire T-DNA  
30 of pGA470 and a broad host range replicon; pJTS222; pJTS250, a binary plasmid that includes HYG<sup>R</sup> constructed by ligation of four fragments, including 353-bp PstI-BamHI fragment encoding part of the hph coding region, 670-bp PstI fragment encoding the remainder of the hph  
35 coding region, 1180-bp NaeI-BamHI fragment constituting T<sub>phas</sub> and pJTS222 digested with BamHI; pUC19B2-P<sub>nos</sub>; pUC19B2+hph-T<sub>phas</sub>; p<sub>nos</sub>-hph-T<sub>phas</sub> expression cassette; and pGA482G (Dr. G. An).

The pGA482Δ+HYG<sup>R</sup> was constructed as follows: SalI fragments of pGA470 were ligated into SalI-digested pBR322. The resulting construct, pJTS262, is comprised of the entire T-DNA of pGA470 (from right to left border) and a second fragment containing part of the broad host range replicon. The 345-bp BclI-BamHI fragment of the resulting plasmid, having the nopaline synthase promoter (P<sub>nos</sub>) fused to the 5' 42-bp of nopaline synthase (14 N-terminal amino acids), was inserted into the BamHI site of pUC19B2, having the SmaI site of pUC19 converted to a BglII site. The resultant recombinant plasmid, pUC19B2+P<sub>nos</sub>, had the P<sub>nos</sub> segment within the BamHI-BglII fragment.

15 A 2.2-kb BamHI fragment containing the *hph* coding region from bacterial transposon Tn5 and the phaseolin transcription terminator (*hph*-T<sub>phas</sub>) was isolated from pJTS250. The 2.2-kb *hph*-T<sub>phas</sub> fragment was inserted into the BamHI site of pUC19B2. The pUC19B2-P<sub>nos</sub> was digested with BamHI and HindIII. pUC19B2+*hph*-T<sub>phas</sub> was partially digested with BamHI and completely with HindIII to produce a 2.2-kb fragment with BamHI-HindIII ends. The fragment was ligated with BamHI-HindIII digested pUC19B2-P<sub>nos</sub> plasmid. The resulting construct, a P<sub>nos</sub>-*hph*-T<sub>phas</sub> expression cassette, pUC19B2+HYG<sup>R</sup>, was partially digested with BamHI; a resulting 5.3-kb fragment was digested with BglII to produce a 2.6-kb fragment. Separately, HindIII-EcoRI-digested pGA482 was ligated with HindIII-EcoRI-digested pSL1180, lacking a mcs.

30 The resulting construct was further restricted to delete 2.5-kb of the original T-DNA containing the mcs. This binary was digested with BglII and ligated with the BamHI-BglII-ended 2.6-kb P<sub>nos</sub>-*hph*-T<sub>phas</sub> fragment to produce pGA482Δ+HYG<sup>R</sup>.

35



**Example 3 Geminivirus DNA Insertion into  
Expression Vector Constructs**

**5 Example 3.1 Synthesis of Wild-Type  
ToMoV-FL AC1 ORF**

ToMoV was collected from infected tomato plants in Bradenton, Florida and inoculated into *Nicotiana benthamiana* and tomato. DNA was isolated from infected  
10 plants and viral DNA was isolated by preparative agarose gels. Viral DNA was digested with BglII, inserted into BglII-digested pSP72 to produce a full-length A-component clone (Seq ID 17). Similarly, a full-length DNA-B clone was produced from viral DNA  
15 digested with BamHI and inserted into BamHI-digested pBluescript II KS+ (Seq ID 18). DNA of either clone inoculated into *N. benthamiana* produced symptoms similar to the original virus.

20 A dimer clone in which DNA-A was inserted as a direct, tandem duplicate into the cloning vector was made by removing the single insert from its original vector with BglII and reinserting it into BglII-digested pSP72. The ApaI fragment of the resulting plasmid  
25 comprising the cloned DNA-A was inserted into the ApaI site of pBluescript II KS+.

**Example 3.3 Synthesis of ToMoV-AC1**

Wild type AC1 sense ORF and antisense (as) ORF of Table  
30 1A were constructed from the AC1 ORF (SEQ ID 1 and 2) and part of the intergenic region was amplified by PCR from ToMoV-infected *N. benthamiana* DNA using primers PFL-2549B (SEQ ID 9) (5'-GGATCCGAGTAACTCATCTGGAGTACC-3') and PFL-1108B (SEQ ID 10)  
35 (5'-GGATCCGGAAGTAGATGGAGCACCCGC-3'). The 1.1-kb PCR product was BamHI-digested and inserted into the BamHI site pBluescript II KS+ to produce pTFAC1.

**Example 3.4 Synthesis of ToMoV-AC1dlm**

For the production of the mutated ORF, the AC1 ORF and part of the intergenic region was PCR amplified from ToMoV-infected *N. benthamiana* DNA by PCR using primers

- 5 PFL-2549H (SEQ ID 16)  
 (5'-TATCAAAGCTTGAGTAACTCATCTGGAGTACC-3') and PFL-1108B  
 (SEQ ID 10) (5'-TATCGGATCCGGAAGTAGATGGAGCACCCGC-3') to  
 produce a HindIII site near the translation start codon  
 and a BamHI site near the translation terminator codon.
- 10 The HindIII-BamHI-digested product was ligated with  
 HindIII-BamHI-digested pBluescript II KS+ in a sense  
 orientation relative to the f1 origin of replication.  
 Mutations were generated in the NTP binding motifs of  
 AC1 of this clone.
- 15
- Trans-dominant lethal mutants (dlm) of AC1 protein (SEQ  
 ID 3 and 4) were created by Kunkel mutagenesis. The  
 above pBluescript plasmid was transformed into CJ236  
 (Invitrogen Co.), a *dut-*, *ung-* strain, so that the
- 20 amplified plasmid DNA contains uracil. Single-stranded  
 DNA was produced by transfecting the above transformed  
 cells with helper phage M13-K07. The complementary  
 sense strand of the ssDNA was synthesized in vitro  
 using deoxynucleotides, including dTTP, and two
- 25 mutagenic primers: PFAC1-680c (SEQ ID 11)  
 (5'-CAAGAACAGGGcAcACGATGTGGG-3') and PFAC1-781c (SEQ ID  
 12) (5'-GTATAACGTCATTaAtACATCGCACCGC-3'). The lower  
 case letters indicate altered nucleotides. The product  
 was treated with T4 DNA ligase and transformed into XL1
- 30 Blue *E. coli* (Stratagene) to amplify plasmids  
 containing the mutations produced by the mutagenic  
 primers, which resulted in the mutations 2(a), 3(b) and  
 3(c), described above.

35 **Example 3.5 Synthesis of ToMoV-AC1dlm1**

The 1.1-kb BamHI fragment of pTFAC1, containing wild  
 type AC1 ORF, was inserted to the BamHI site of pRT101e  
 to produce a sense (pRTAC1-S) construct. The AC1  
 triple mutant (AC1 dlm) ORF was removed as a 1.1-kb

XhoI-BamHI fragment from its vector and inserted in the sense orientation into XhoI-BamHI-digested pRT101e to produce pRT101e+AC1dlm. Plasmids pRTAC1-S and pRT101e+AC1dlm were cleaved at the unique PmlI site.

5 After an additional digestion with ScaI, 1.6- and 3.2-kb fragments were isolated from each digest. The 1.6-kb fragment from pRTAC1-S was ligated with the 3.2-kb fragment from pRT101e+AC1dlm to produce a construct comprising the sequence designated as ToMoV-AC1dlm1

10 (SEQ ID 5 and 6) in Table 1A, mutation 2a described above.

#### Example 3.6 Synthesis of ToMoV-AC1dlm23

Plasmids pRTAC1-S and pRT101e+AC1dlm were cleaved at the unique PmlI site. After an additional digestion

15 with ScaI, 1.6- and 3.2-kb fragments were isolated from each digest. The 3.2-kb fragment from pRTAC1-S was ligated with the 1.6-kb fragment from pRT101e+AC1dlm to produce a construct comprising the sequence designated

20 as ToMoV-AC1dlm23 (SEQ ID 7 and 8) in Table 1A, double mutations 3(b) and 3(c) described above.

#### Example 3.7 Synthesis of ToMoV-AC1-AC2-AC3

A construct containing the AC1-AC2-AC3 fragments was produced by ligating a BamHI-HindIII fragment of a

25 binary plasmid comprised of a dimer of the full-length, infectious ToMoV A-component with BamHI-HindIII-digested pJTS222. The BamHI-HindIII fragment from this construct was inserted into BamHI-HindIII-digested

30 pBluescript II KS+. A 1.24 kb BglII-SphI fragment of the resulting plasmid, containing the complete AC2 and AC3 coding sequences and the C-terminal two-thirds of the AC1 ORF (SEQ ID 15), was ligated into BglII-SphI-digested pSL1180. The resulting plasmid contained the

35 AAC1-AC2-AC3 fragment from ToMoV-A.

**Example 4. TYLCV-IS-EG Wild Type and Mutant Sequences.****Example 4.1 Synthesis of TYLCV-C1**

Tomato leaves with TYLCV symptoms were collected in  
5 Fayoum, Giza and Ismailia, Egypt. They were grafted to  
Geneva 80 tomatoes and *N. benthamiana*. The tomatoes  
and tobacco developed symptoms typical of TYLCV.  
Infectious TYLCV (TYLCV-IS-EG1) DNA was isolated from  
the infected *N. benthamiana*. The C1 ORF of TYLCV-IS-  
10 EG1 (SEQ ID 19 and 20) was produced as a 1.1-kb  
fragment by PCR amplification of infected plant DNA.  
The primers used were pTYIRC4 (SEQ ID 21) (5'-  
GGCCATAGAGCTTTGAGGGATCC CGATTCATTTC-3') and PTYC2v1679  
(SEQ ID 22) (5'-GGTAGTAT GAGGATCCACAGTCTAGGTCT-3').  
15 After BamHI-digesting the PCR products, they were  
ligated with BamHI-digested pBluescript II KS+ to  
produce pEGAL1-AS1, which contained the C1 ORF, as  
TYLCV-C1.

**20 Example 4.2 Synthesis of TYLCV-AC2as**

A truncated C2 ORF ( $\Delta$ C2) was produced as a 365 bp  
fragment by PCR amplification of TYLCV-IS-EG1-infected  
*N. benthamiana* DNA. The primers PTYC2v1499 (SEQ ID 32)  
(5'-ATTTGTGGATCCTGATTACCTTCCTGATGTTGTGG-3') and  
25 PTYC2c1814 (SEQ ID 35) (5'-AAACGGATCCTTGAAAAATTGGGC-3')  
were used. The primers were BamHI-digested and ligated  
into BamHI-digested pBluescript II KS+ to produce  
pTYC2-25-1, which contained the  $\Delta$ C2 ORF in antisense  
orientation.

30

**Example 4.3 Synthesis of TYLCV-V1**

A truncated V1 ORF was produced as a 625-bp fragment by  
PCR amplification of TYLCV-IS-EG1 infected *N.*  
*benthamiana* DNA. The primers used were PTYAR1v466 (SEQ  
35 ID 33) (5'-TTAGGATCCTATATCTGTTGTAAGGGC-3')  
and PTYAR1c1046 (SEQ ID 34)  
(5'-TTAACTAATGCAGGATCCTACATTCCAGAGGGC-3').

The primers were BamHI-digested and ligated into BamHI-digested pBluescript II KS+ to produce pTYV1-6-1, which contains the V1 ORF.

5           Example 4.4   Synthesis of TYLCV-C1-AC2-AC3

A 1.3-kb fragment of the TYLCV-IS-EG1 genome from nt 1471 to nt 20 via nt 2787 (Navot et al 1991) was produced by PCR amplification of infected *N. benthamiana* DNA. The primers used were PTYIRc4 and  
10 PTYC2v1499. The primers were BamHI-digested and inserted into BamHI-digested pBluescript II KS+ to produce pTYEGC4.

          Example 4.5   Synthesis of TYLCV ORF Mutations

15 A full-length infectious clone of TYLCV-IS-EG1 (pTYEG14) was created to serve as the basis for TYLCV ORF constructs and for agroinoculation (see below). DNA from a tomato infected with TYLCV-IS-EG1 was used as template in two PCR amplification reactions. The  
20 first used primers PTYC1c2196 (SEQ ID 37) (5'-AAATCTGCAGATGAACTAGAAGAGTGGG-3') and PTYV1v1164 (SEQ ID 36) (5'-GTACGAGAACCATACTGAAAACGCCT-3') to amplify a fragment. The PstI-SphI-digested fragment was ligated with PstI-SphI-digested pGEM-5zf+ (Promega)  
25 to produce plasmid pEG11A.

The second amplification reaction employed primers PTYC1v2182 (SEQ ID 39) (5'-TAGGCCATGGCCGCGCAGCGGAATACACG-3') and PTYC3c1320  
30 (SEQ ID 38) (5'-GGTTCTGCAGCAGAGCAGTTGATCATGTATTG-3'). The PstI-NcoI-digested fragment was ligated with PstI-NcoI-digested pGEM-5zf+ to produce pEG11-7B.

To assemble the full-length virus, the PstI-NcoI  
35 fragment of pEG11-7B was ligated with the PstI-NcoI fragment of pEG11A to produce a construct comprising full-length 2.7-kb viral DNA. The full-length construct was tested for infectivity by biolistic delivery into tobacco cells and found to create

symptoms identical to the original disease. This clone was called pTYEG14. Orientation of insertion with respect to the f1 origin of replication was confirmed by DNA sequencing.

5

Three mutant C1 ORFs were constructed, each having one or two base changes altering the amino acid specificity of one codon by Kunkel mutagenesis using the plasmid representing the full-length infectious clone of TYLCV-  
10 IS-EG1 (pTYEG14) as template. The mutagenic primers (all viral sense) were:  
PC1v2467 (SEQ ID 25) (5'-GTTTCCGTCTcgCTCCACGTAGG-3');  
PC1v2101 (SEQ ID 28) (5'-GGCCCACATTGTTgCGCCTGTTCTGC-3'); and PC1v2000 (SEQ ID 31)  
15 (5'-GGGTCTACGTCTctAATGACGTTGTACC-3'). (Lower case letters indicate altered nucleotides.) The resulting DNA was treated with T4 DNA ligase and transformed into XLI Blue *E. coli* cells to produce the following constructs: pTYK<sup>104</sup>R #1 (SEQ ID 23 and 24), mutation  
20 1(c); pTYK<sup>223</sup>A #4 (SEQ ID 26 and 27), mutation 2(b); and pTYD<sup>259</sup>R #5 (SEQ ID 29 and 30), mutation 3(a), described above.

The three mutant C1 ORFs were cloned into pCRII  
25 (Invitrogen). The C1 ORF for each mutant was PCR amplified using primers PTYIRc4 (SEQ ID 21) (5'-GGCCATAGAGCTTTGAGGATCCCGATTCAATTC-3') and PTYCV1707 (SEQ ID 42) (5'-GGTAGTATGAGGATCCACAGTCTAGGTCT-3'). The amplified fragments were ligated with pCRII to produce:  
30 pC1K<sup>104</sup>R #2, mutation 1(c); pC1K<sup>223</sup>A #4, mutation 2(b); and pC1D<sup>259</sup>R #2, mutation 3(a), described above.

These three ORF in BamHI fragments of their respective vectors provided the mutant C1 ORFs for expression  
35 cassettes for *Agrobacterium* mediated transformation.

**Example 5 BGMV Constructions**

Wild-type and mutated versions of BGMV C1 (replication protein) ORF have been prepared. The wild-type sequence (SEQ ID 43 and 44) was mutated by Kunkel mutagenesis. Mutations in BGMV-C1 disclosed here include:

ORF	Mutant	SEQ ID	Mutagenic Primer
BGAC190	control	45	47
BGAC221	mutation 2(c)	48	50
BGAC228	mutation 2(a)	51	53
BGAC262	mutation 3(a)	54	56

SEQ ID NOS. 45, 48, 51, and 54, refer to mutagenized BGMV-C1 ORF DNA sequences presented in the Sequence Listing. These encode protein sequences 46, 49, 52, and 55, respectively. The mutant sequences were derived from wildtype DNA by Kunkel mutagenesis with mutagenic primers 47, 50, 53, and 56, respectively.

A 1.8Kb BamHI-XhoI fragment containing the 35S promoter transcriptionally fused to a mutated AC1 ORF from BGMV-GA followed by the nopaline synthase transcription terminator was removed from WRG2398 (Dr. D. R. Russell, Agracetus Corp., Middleton, WI). The AC1 coding sequence was mutated in vitro using Kunkel mutagenesis to produce double mutations 2(c) and 2(a). This fragment was ligated with pRT101e digested with the same enzymes and the ligation mix used to transform *E. coli* DH5 cells. Some transformants yielded desired recombinant plasmids that had the entire expression cassette from WRG2398 inserted into PRT101e (pJTS364). The new expression cassette was removed as a 2.9-Kb fragment from one of the recombinant plasmids by partial digestion with HindIII. It was ligated with pJTS246Δ that has been digested with HindIII and treated with CIAP. After transformation of DH5 cells, one recombinant among the transformants was identified that had the expression cassette inserted in the binary

vector. DNA of this binary vector was transformed into *A. tumefaciens* LBA4404 and one transformant containing the binary was called strain At<sup>364</sup>.

- 5 Plasmid pJTS364 was digested with EcoRV to eliminate the duplicated 35S promoters (P<sub>35S</sub>) and the cleaved DNA ligated. A fraction of the rejoined molecules have a deletion for the fragment between the EcoRV sites which contains the 35S enhancer (e<sub>35S</sub>) from WRG2398 and P<sub>35S</sub>  
10 from pRT101e. The ligation mix was used to transform DH5 cells. Among the transformants, the desired deleted plasmid was found and called pJTS365. The 2.5-Kb expression cassette was removed and ligated with HindIII-digested, CIAP treated pJTS246Δ. The ligation  
15 mix was used to transform DH5 cells. Recombinant binary plasmids were identified among the transformants and one of these was used as a source of DNA which was transformed into *A. tumefaciens* LBA4404. The transformed agrobacterium having the recombinant binary  
20 was called At<sup>365</sup>.

The listed BGMV ORF are installed into appropriate promoter vectors and then into binary plasmids for *Agrobacterium*-mediated transformation into *Phaseolus*  
25 plants. Additionally, expression vectors are delivered into plants by biolistic acceleration or other methods by which plants can be transformed. Regenerated transformed plants are evaluated for levels of transgene RNA accumulation by RNA blot analysis to  
30 verify activity of the transgene. Subsequently, progeny are evaluated for ability to resist BGMV infection.

35           **Example 6   Expression Cassettes and  
                  *Agrobacterium* strains.**

The following ToMoV constructs were produced.



#### Example 6.1 RTSC and RTAC

The 1.1-kb BamHI fragment of pTFAC1, containing wild type AC1 ORF was inserted to the BamHI site of pRT101e. Antisense (pRTAC1-A) and sense (pRTAC1-S) constructs were produced. HindIII fragments of each plasmid were each inserted into the HindIII site of pJTS246A in the same transcriptional direction as the NPTII selectable marker. The binary vectors were transformed into LBA4404 to produce RTAC (antisense) and RTSC (sense).

#### Example 6.2 DHSC and DHAC

The wild type AC1 ORF was also inserted as a BamHI fragment into BamHI-digested pDH51 in both orientations creating pDHAC1-S (sense) and pDHAC1-AS (antisense). The expression cassette of each recombinant was removed with EcoRI and inserted into EcoRI-digested pJTS235. Recombinant binary plasmids were selected that had the expression cassette inserted such that the directions of transcription as the selectable marker. These binary plasmids were introduced into LBA4404 by transformation to produce DHSC (sense) and DHAC (antisense).

#### Example 6.3 RTSFS

pRTAC1-S was digested with BglII and flush ended by filling out. The resulting plasmid, pRTAC1-SABglII, lacked a BglII site but retained a core 4-base Sau3A site. This mutation shifted the translation reading frame by adding four nucleotides thereby producing a translation stop codon, and truncating the polypeptide (SEQ ID 13 and 14). A 2.1-kb HindIII fragment of pRTAC1-SABglII, which contains the expression cassette, was inserted in both orientations into the HindIII site of pJTS246A, unidirectional or divergent respecting the sense of selectable marker. A plasmid having an unidirectional orientation was introduced into LBA4404 by transformation to produce RTSFS.

**Example 6.4 RT3AA**

The 1.24-kb BglII-KpnI fragment of pSL1180+ΔAC1-AC2-AC3 was ligated into BglII-KpnI-digested pRTAC1-A to produce, pRT3AA, a pRT101e-like construct with the AC1, AC2 and AC3 ORFs inserted in antisense orientation. The 2.7 kb HindIII fragment of the pRT3AA was inserted into the HindIII site of pJTS246Δ in unidirectional orientation. The construct was introduced into LBA4404 by transformation to produce RT3AA.

10

**Example 6.5 LASD and LASU**

The 600-bp EcoRI-HincII fragment of pSL1180+PLAT52 was ligated with EcoRI-HincII-digested pRTAC1-S to replace the 800-bp 35S EcoRI-HincII promoter fragment by the 600-bp LAT52 EcoRI-HincII promoter fragment. After linearizing the plasmid with NcoI, the ATG start codon was destroyed by mung bean nuclease. The resulting plasmid contained an EcoRI and HindIII, but lacked a NcoI site. Accordingly, the sequences flanking the mutated NcoI site were the same as in the original LAT52 promoter untranslated 5' leader. The 5' untransformed leader was lengthened to 181 bp and included 68% A/T nucleotides. HindIII cut plasmid fragment containing the expression cassette was inserted into the HindIII site of pJTS246Δ in both unidirectional and divergent orientations respecting the sense of the selectable marker. One binary of each type was transformed into LBA4404 creating strains LASU and LASD, respectively.

20  
25  
30**Example 6.6 MEU and MEU2**

The AC1 triple mutant (d1mAC1) ORF was removed as a 1.1-kb Xho I-BamHI fragment from its vector and inserted in the sense orientation into Xho I-Bam HI-digested pRT101e. A 2.1-kb expression cassette thus created was removed from pRT101e+AC1d1m by incompletely digesting the recombinant vector with HindIII and isolating a 2.1-kb fragment. This fragment was inserted into the HindIII site of pJTS246Δ to produce a

mutated enhanced unidirectional (MEU) vector. A second binary involving the same expression cassette which was tandemly duplicated in the unidirectional orientation was called MEU2. Both of the above binary vectors were  
5 transformed into LBA4404 to produce MEU and MEU2, respectively.

#### Example 6.7 MUA and MUB

ToMoV-AC1dlm1 was partially digested with HindIII and  
10 the 2.1-kb expression cassette was isolated.  
ToMoV-AC1dlm23 was completely digested with HindIII and the 2.1-kb cassette isolated. Each cassette was inserted into the HindIII site of pJTS246Δ. The recombinants were transformed into LBA4404 creating the  
15 *Agrobacterium* strains MUA and MUB, respectively.

#### Example 6.8 MUAIN and MUBIN

The 1.2 kb XhoI-BamHI-fragment of pRT101e+AC1 dlm1 containing the AC1dlm1 ORF was ligated with the XhoI-  
20 BamHI-fragment of pRTIN+Geneblock in a sense orientation. This construct was incompletely digested with HindIII followed by complete digestion with ScaI to produce a 2.6-kb fragment comprising the expression cassette. They were ligated with HindIII-digested  
25 pJTS246Δ in a divergent orientation respecting the selectable marker. The resulting *Agrobacterium* strain was called MUAIN.

The 2.1 kb BamHI fragment of pRT101e+ AC1dlm23,  
30 containing the AC1dlm23, was ligated with BamHI-digested OpRTIN+Geneblock plasmid in the sense orientation. This plasmid was digested with HindIII and ScaI producing a 2.6-kb expression cassette fragment which inserted into HindIII-digested pJTS246Δ  
35 in an unidirectional direction. Plasmid DNA from this clone was transformed into LBA4404 to produce MUBIN.

**Example 6.9 CODLM**

The 1.1 kb BamHI fragment containing the wild type AC1 ORF was inserted into the BamHI site of pΔ1CO35 in a sense orientation to produce pΔ1CO35+AC1S. The 4.5 kb  
5 ApaI-BglIII fragment of pΔ1CO35+AC1S was restricted to delete a 475-bp comprising wild-type AC1 ORF and ligated to the ApaI-BglIII fragment of pRT101e+AC1 dlm1 to replace the wild type internal fragment by the mutated fragment. The recombinant (pΔ1CO35+AC1 dlm)  
10 was incompletely digested with HindIII, the 2.4-kb fragment containing the expression cassette isolated and inserted into the HindIII site of pJTS246Δ in an unidirectional orientation. The plasmid was transformed into LBA4404 cells to produce CODLM.

15

**Example 7 Constructs Containing TYLCV-IS-EG1****Example 7.1 LCA**

The 1.1 kb BamHI fragment of pEGAL1-AS1 containing the  
20 C1 ORF was inserted in the BamHI site of pRT101e in an antisense orientation to produce pRTLCA1-A. A 2.1 kb HindIII fragment of pRTLCA1-A was inserted into the HindIII of pJTS246Δ in the unidirectional (U) orientation with regard to directions of transcription.  
25 LBA4404 cells were transformed with the resulting plasmid to produce LCA.

**Example 7.2 LCR'**

A 350-bp BamHI fragment encoding part of the C2 ORF of  
30 TYLCV-IS-EG1 was removed from pTYC2-25-1 and ligated into the BamHI site of pRT101e. The resulting construct contained the truncated C2 ORF inserted in an antisense orientation with respect to P<sub>35S</sub>. The 1.3-kb expression cassette removed by HindIII digestion was  
35 inserted into the HindIII site of pJTS246Δ. Plasmid DNA of the resulting recombinant was partially digested with HindIII and ligated with the C1 antisense expression cassette. The desired plasmid had one copy of each the expression cassett inserted such that the

directions of transcription of all cassettes was unidirectional. DNA of this binary plasmid was transformed into LBA4404 to produce a strain, LCR', comprising the two-cassette recombinant binary plasmid.

5

#### Example 7.3 LCR''

A 620-bp BamHI fragment of pTYV1-6-1 encoding part of the V1 ORF of TYLCV-IS-EG1 was ligated into the BamHI site of pRT101e in an antisense orientation with respect to the 35S promoter. A HindIII fragment of the resulting plasmid was ligated into the HindIII site of pJTS246A in an unidirectional direction respecting the selectable marker. Plasmid DNA of this recombinant was transformed into LBA4404 to produce LCR''.

15

#### Example 7.4 RT3CA

The 1.3 kb BamHI fragment of pTYEGC4 containing the C1+AC2+AC3C structure was inserted into the BamHI site of pRT101e in an antisense manner with respect to the direction of transcription of the 35S promoter. The 2.3-kb HindIII fragment of pTYEGC4 the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246A in an unidirectional transcription directions. LBA4404 transformed with this plasmid to produce strain RT3CA.

The 1.3 kb BamHI fragment of pTYEGC4 comprising C1+AC2+AC3 DNA was ligated into the BamHI site of pA1Co35 in an antisense orientation with respect to the Commelina yellow mottle virus promoter. The 2.8 kb HindIII fragment of the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246A in an unidirectional orientation respecting the selectable marker. Plasmid DNA transformed into LBA4404 produced CO3CA.

The mutated 1.2 kb fragments containing C1 ORF were removed from their pCRII vectors and directionally ligated into the EcoRV-HindIII fragment of eP<sub>ma</sub>-mcs-T<sub>phai</sub>.

The resulting constructs were digested with XhoI and NaeI. HindIII fragments of pGA482Δ+HYG<sup>R</sup> were flush ended by filling out, and digested with XhoI. The XhoI-NaeI expression cassettes were ligated into the  
5 binary vector that had an XhoI cohesive end and a blunt end to produce three constructs, C<sup>104</sup>, C<sup>225</sup> and C<sup>259</sup>. DNA of each of the constructs were transformed into LBA4404 to produce the strains LC104, LC225 and LC259 and into *Agrobacterium* strain EHA105 (Mogen International, N.V.)  
10 to produce strains EC104, EC225 and EC259.

#### Example 7.5 RT3CS

The 1.3 kb BamHI fragment of pTYEGC4 containing the C1+ΔC2+ΔC3C structure was inserted into the BamHI site  
15 of pRT101e in an sense manner with respect to the direction of transcription of the 35S promoter. The 2.3-kb HindIII fragment of pTYEGC4 the resulting plasmid containing the expression cassette was inserted into the HindIII site of pJTS246Δ in an unidirectional  
20 transcription directions. LBA4404 transformed with this plasmid to produce strain RT3CS.

#### Example 8. Production of Transgenic Plants Containing Disclosed Constructions and 25 Analysis of Transgene Expression

Transgenic plant were produced by *Agrobacterium*-co-cultivation procedures well known to those skilled in the art.

30 The media of compositions used are here defined, for 1 liter:

1/2X basal: 1/2X MS salts (Gibco), 10 g sucrose, 7 g agar, pH 5.8;

TCM: 1X MS salts, 30 g sucrose, 0.2 g KH<sub>2</sub>PO<sub>4</sub>, 1X  
35 N&N vitamins (Gibco), 0.1 mg 2,4-D, 0.05 mg kinetin, 20 mg acetosyringone, 7 g agar, pH 5.8

1Z: 1X MS salts, 30 g sucrose, 1X N&N vitamins, 1 mg zeatin, 100 mg kanamycine sulfate, 500 mg carbenicillin, 7 g agar, pH 5.8;

TR1: 1X MS salts, 30 g sucrose, 1X N&N vitamins,  
3 mg glycine, 0.17 g  $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ , 40 mg acetosyringone,  
pH 5.8;

5 MK5: 1/2X MS salts, 10 g sucrose, 1X N&N  
vitamins, 3 mg glycine, 0.17 g  $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ , 50 mg  
kanamycin sulfate, 500 mg carbenicillin, 7 g agar, pH  
5.8;

C: 1X MS salts, 30 g sucrose, 1X N&N vitamins,  
3 mg glycine, 0.8 g  $\text{NH}_4\text{NO}_3$ , 2 mg BAP, 0.5 mg IAA, 100 mg  
10 kanamycin sulfate, 250 mg carbenicillin, 7g agar, pH  
5.8.

Seeds were sterilized by briefly rinsing in 70% EtOH  
and then in a solution of 20% chlorox plus Tween-20.  
15 The seeds were dried in vacuo and then rinsed several  
times with sterile water. Washed seeds were  
transferred into 1/2X basal media and incubated in a  
Magenta box for about 7 days in 16 hour photoperiods  
daily.

20 Fully expanded cotyledons were cut aseptically under  
water. Two cuts were made at the end, and the tip of  
the cotyledon piece and the center piece was retained  
and used. A culture of *Agrobacterium* containing the  
25 appropriate binary plasmid was initiated 24 hours  
before co-cultivation. Bacteria in 4-5 ml of the  
culture were collected by centrifugation and  
resuspended in TR1-liquid media. The suspension was  
poured onto cut cotyledon pieces and incubated for  
30 about 25 min. The cotyledon pieces were placed on  
sterile filter papers and placed compactly on TCM  
medium. The plates were kept in the dark at room  
temperature for about 48 hours, after which they were  
placed on plates containing 1Z medium. The plates were  
35 incubated in 16 hours light daily at about 24° C for  
about 21 days.

Calli that formed on cotyledon pieces were transferred  
to fresh 1Z plates and shoots were removed as they

formed to 1/2-X MK-5 tubes for rooting. A 4-mm piece of leaf from the shoot was also placed on C medium for callus formation. Twelve to fourteen days after the plating on C medium, calli were scored as "-" or "+".

- 5 About 60 to 70% of shoots with + callus root in MK5 media. Those that have + callus but did not root were trimmed off at the end and re-rooted on fresh MK5 tubes. About 80% of these will root on the second attempt.

10

Rooted shoots were removed to potting soil when a strong root system has developed, usually about 3 weeks after rooting. The plants were kept in a closed plastic bags for about 3 days, the bags were opened

- 15 slowly after that to acclimatize the young plant. A 6- to 8-mm piece of leaf tissue was collected for the NPTII ELISA assay. The NPTII positive plants were transferred to the greenhouse for seed production. About 4 to 5 weeks in the greenhouse leaf tissues were  
20 collected for RNA isolation and Northern blots were done for these plants.

#### Example 9. Analysis of Transgenic Plants

- Transgene RNA expression in transgenic tomato lines was  
25 accomplished by estimating steady state transcription levels using Northern blot hybridization. The level of transgene expression was used to select lines for agroinoculation. Total RNA was isolated from leaves and stems of young plants and electrophoresed on  
30 agarose gels.

The appropriate ORF DNA probe was radio-labeled and hybridized to RNA blotted on paper. After washing the RNA was visualized by autoradiography on X-ray film.

35

The following Tables 2, 3, and 4 summarize results showing plants produced with geminivirus constructs described above. The following symbols are used:

No+ or No-, Northern blot positive or negative;



So+ or So-, Southern blot positive or negative;

\*, no data;

R<sub>0</sub> and R<sub>1</sub>, primary and progeny lines.

Table 2 summarizes the transgenic tomato plants

5 produced by transfer of wildtype ToMoV ORF DNA into the plant by Agrobacterium infection. For example, several tomato plants (TGM-1 to -17, -20, -24, -28, -29, -33 to -41, -47 to -49, -53, -54, -59 to -67, -70 to -131; TTGV92-1 to -5, -10, -13 to -20) were produced by  
10 Agrobacterium containing the RTAC construct. As shown in Table 1A, this construct is comprised of the ToMoV AC1 ORF in an antisense configuration. The predominant characteristic of these RTAC-containing plants is the presence of ToMoV DNA in the plant tissue (i.e., So+),  
15 transcribed RNA (i.e., No+), and transmitted these traits to their progeny (R, RNA). Table 2 also described transgenic plants with DHAC and RT3AA constructs, comprised of ToMoV AC1 and AC1-AC2-AC3 antisense ORF, respectively (Table 1A).

20

Table 3 describes transgenic tomato plant containing mutant ToMoV ORF. These include the meu, meu2, Codlm, mub, mua, mubin, mauin, rtsfs, lasu, and lasd constructs described in Table 1A.

25

Table 4 describes transgenic tomato plant containing TYLCV ORF. These include LCA, LCR, RT3CA, RT3CS and Co3CA constructs of Table 1A, comprising TYLCV C1, C2 and C3 ORF.

30

These results establish that the methods described herein produce transgenic plants using DNA constructs containing gemini virus ORF.

TABLE 2

## TOMATO PLANTS TRANSFORMED WITH ToMoV

	Product	Gene	R <sub>0</sub> RNA	R <sub>1</sub> RNA	R <sub>0</sub> DNA
5	Tgm-1, 10, 12, 14, 20, 29, 39, 53, 54, 64, 66, 70, 71, 80, 81, 82, 127	RTAC	No+	No+	So+
	Tgm-3, 8, 13, 16, 17, 24, 28, 33, 34, 36, 40, 41, 47, 48, 49, 65, 114	RTAC	*	*	So+
10	Tgm-35	RTAC	*	*	So-
	Tgm-59, 79, 102, 88, 116	RTAC	No-	No-	So+
	Tgm-67	RTAC	No+	No-	So+
15	Tgm-84, 90, 93, 94, 97, 98, 99, 100, 101, 103, 106, 107, 108, 112, 113, 115, 117, 120, 121, 122, 123, 125, 129, 131	RTAC	No+	*	So+
	Tgm-18, 19, 26, 42, 55, 58, 68	DHAC	*	*	So+
	Tgm-23, 31, 44, 51	DHAC	No+	No+	So+
	Tgm-27	DHAC	No-	No+	So+
	3AA-3, 7, 9, 12, 13, 18, 21, 22, 23, 26, 27, 30	RT3AA	No+	*	*
20	3AA-4, 11, 16	RT3AA	No-	*	*
	TTGV92-1	RTAC	No+	No-	So+
	TTGV92-2, 5, 15, 17	RTAC	No-	*	So+
	TTGV92-3, 13, 19	RTAC	No-	*	So-
	TTGV92-4, 20	RTAC	No+	No+	So+
25	TTGV92-6, 20	DHAC	No+	No+	So+
	TTGV92-7	DHAC	*	No+	So+
	TTGV92-10	RTAC	No+	No+	*
	TTGV92-11	DHAC	No+	*	So+
	TTGV92-14	RTAC	No-	*	*
30	TTGV92-16	RTAC	*	*	So-

TABLE 3

**TOMATO PLANTS TRANSFORMED WITH ToMoV  
REP ORF DOMINANT LETHAL MUTANT CONSTRUCTS**

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Product	Construct	R <sub>0</sub> RNA	R <sub>1</sub> RNA
TTGV92-26, 28, 36	meu2	*	*
TTGV92-27	meu2	No-	*
TTGV92-42	meu2	*	No+
DLM2, 39, 42, 46, 47, 48, 49, 51, 52, 55, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 79, 80, 81, 82, 83, 85, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 104, 106, 107, 108, 109, 110, 112, 116, 117, 118, 119, 120, 122, 124, 126, 127, 130, 133, 135, 136, 137, 139, 144, 148, 149, 151, 180, 155, 159, 162, 167, 170, 172, 173, 177, 192, 198, 200, 201, 204, 206, 211, 215, 217, 219, 220	meu	No+	*
DLM3, 5, 7, 9, 10, 12, 14, 15, 18, 21, 26, 30, 31	meu	No+	No+
DLM16	meu2	No-	No-
DLM17, 29	meu	*	*
DLM22	meu	No-	No-
DLM24	meu	No-	No-
DLM25	meu2	No+	No+
DLM27, 28	meu	No-	No-
DLM32	meu2	No+	No+
DLM37, 38, 44, 57, 59, 61, 75, 115, 129, 131, 138, 150, 166, 174, 179, 189, 208	meu	No-	*
DLM143	meu	No-	*
CODLM2, 4, 5, 6, 8, 9, 10, 13, 14, 15, 16, 18, 21, 24, 26, 28	Codlm	No+	*
CODLM3, 7, 19, 27	Codlm	No-	*
MU-2, 3, 4, 5, 6, 7, 14, 15, 19, 20, 26, 27, 30, 31, 32, 33, 34, 36, 37	mub	No+	*
MU-8, 9, 12, 16, 18, 22, 28, 39, 41	mua	No+	*
MU-11	mua	No-	*
MU-13, 47	mub	No-	*
MUIN-3, 6, 7	mubin	No+	*
MUIN-4, 5	muain	No+	*
MUIN-8, 10, 11, 14, 17, 18	mubin	*	*

Table 3, cont.

Product	Construct	R <sub>0</sub> RNA	R <sub>1</sub> RNA
MUIN-9, 15, 16, 19	muain	*	*
RTSFS-1, 3, 4, 6, 9, 10	rtsfs	No +	*
RTSFS-7, 8	rtsfs	No -	*
LAS-1	lasu	No +	*
LAS-6, 10	lasd	No +	*
LAS-11	lasd	No -	*

5

TABLE 4

**TRANSGENIC TOMATO PLANTS TRANSFORMED  
WITH TYLCV GENE CONSTRUCTS**

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25

Product	Construct	R <sub>i</sub> DNA	R <sub>i</sub> RNA	R <sub>i</sub> RNA
Lca-1, 2, 37, 39, 43	lca	So-	*	*
Lca-5, 14, 21, 24, 29	lca	So+	*	No+
Lca-6, 35, 36, 46	lca	So+	*	*
Lca-8, 12, 18, 19, 20, 26, 28	lca	So+	*	No-
Lca-25	lca	*	*	No-
Lca-45	lca	So+	No+	*
Lcr-1, 5, 6, 22	lcr	So+	No+	*
Lcr-3, 4, 17, 18, 20, 24	lcr	So-	No-	*
Lcr-12	lcr	So-	No+	*
Lcr-16, 31	lcr	So+	No-	*
Lcr-25	lcr	So+	*	*
Lcr-26, 27, 29, 32	lcr	So-	*	*
3CA-2, 3, -4, -6, -12, -15, -17, -18, -19, - 21, -22	RTJCA	*	No+	*
CO3CA-1, -2, -4, -5, -7, -8, -9, -11, -12, - 13, -14, -17, -18, -19	Co3CA	*	No+	*
CO3CA-6, -10	Co3CA	*	No-	*
RT3CS-1	RT3CS	*	No-	*

## Example 10. Viral Challenge of Transgenic Plants

### 5 Example 10.1 ToMoV Agroinoculation Vector

A 5.6-kb fragment composed of a dimer of full-length infectious DNA-A was ligated with BamHI-HindIII digested binary plasmid pJTS222 to produce construct comprising the ToMoV-A dimer. The resulting plasmid  
10 produced transformed LBA4404 cells, uses as the A-component in agroinoculation experiments.

A 6.9-kb XbaI fragment that includes a full length infectious clone of DNA-B and the complete pBluescript  
15 II KS+ plasmid was inserted into the XbaI site of pJTS222. The resulting plasmid produced transformed LBA4404 cells used as the B-component in agroinoculation experiments.

### 20 Example 10.2 TYLCV-IS-EG1 Agroinoculation Vector

The full length TYLCV-IS-EG1 DNA from infectious clone pTYEG14 was removed from the plasmid by SphI digestion and inserted at high molar excess into the SphI site of pGEM5Zf+ (Promega). The resulting plasmid, pTYEG7,  
25 contained a dimer of infectious TYLCV-IS-EG1 DNA. The 6.7-kb fragment of ScaI-PstI fragment of pTYEG7 comprised the dimer and part of pGEMZaf+. The 1.9-kb PstI-ScaI fragment of pSL1180 was ligated with the 6.7-kb fragment from pTYEG to produce a 8.7-kb construct  
30 with a single BglII site.

The 7.0 kb ScaI-BamHI fragment of the resulting recombinant plasmid was ligated with HpaI-BamHI-digested pJTS222. A resulting construct was used to  
35 transform LBA4404 cells to produce AtLC1, which was used in the TYLCV agroinoculation experiments.

### 10.3 Agroinoculation Procedure

R<sub>1</sub> plants from self pollinated R<sub>0</sub> primary regenerants were agroinoculated 3 weeks after sowing. For bipartite geminiviruses, agroinoculation involves  
5 delivery of greater-than-full-length (must contain 2 common regions) ToMoV DNA-A and DNA-B into the seedlings using *Agrobacterium*. A small amount of a mixture of two *Agrobacterium* strains each containing a  
10 tandem duplication of infectious geminivirus DNA was injected into the plant. For monopartite geminiviruses, only one agrobacterial strain is required if it carries a binary vector comprising a full or partial duplication of a full length infectious  
15 DNA.

Overnight cultures of *Agrobacteria* were diluted, and injected into stems of one month old tomato seedlings. About 100 hours later, a second inoculation identical  
20 to the first is performed.

Detection of NPTII by ELISA was taken as an indicium of the presence of the transgene. Agroinoculation experiments, summarized in Tables 5 to 10, show an  
25 array of resistance phenotypes. The data show several transgenic tomatoes resistant to ToMoV infection, including DLM12, TTGV92-42, CODLM6, CODLM8, CODLM13, CODLM14, MUA9, MUB20, MUA8, MUA18, MUA28, and MUA41.

Table 5. ToM V Agroinoculations - DLM Transgenics

	Line (Generation)	Days Part Inoculation observation	Fraction of symptom-free and virus-free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
5	TTGV92-36 (R1)	20	2/16	2/16	0/2	0/2
	TTGV92-42 (R1)	20	9/11	8/11	3/7	3/7
	untransformed	20	*	*	0/17	0/17
10	DLM3 (R1)	26	*	5/16	*	0/2
	DLM7 (R1)	26	*	4/15	*	1/3
	DLM9 (R1)	26	*	0/14	*	1/2
	DLM10 (R1)	26	*	2/16	*	0/2
	DLM12 (R1)	26	*	10/17	*	0/1
15	untransformed	26	*	*	*	0/20
	DLM12 (R1)	23	8/11	6/11	*	*
	TTGV92-42-(R2)	23	*	*	3/18	2/18
	TTGV92-42-(R2)	23	6/13	4/13	0/5	0/5
20	TTGV92-42 (R1)	23	13/15	10/15	0/3	0/3
	untransformed	23	*	*	1/24	1/24
	DLM12 (R1)	21	12/20	13/20	1/5	1/5
	DLM14 (R1)	21	6/18	4/18	*	*
	DLM15 (R1)	21	0/14	0/14	0/4	0/4
25	DLM27 (R1)	21	0/15	0/15	0/3	0/3
	DLM28 (R1)	21	1/16	1/16	0/1	0/1
	untransformed	21	*	*	0/15	0/15
	DLM5 (R1)	18	0/13	1/13	0/5	0/5
	DLM17 (R1)	18	1/5	1/5	3/9	3/9
30	DLM22 (R1)	18	0/15	0/15	0/3	0/3
	DLM26 (R1)	18	2/3	2/3	1/5	1/5
	DLM29 (R1)	18	0/13	0/13	1/3	1/3
	DLM30 (R1)	18	3/14	3/14	1/4	1/4
	DLM31 (R1)	18	4/12	4/12	0/6	0/6
35	TTGV92-42-17(R2)	18	7/13	6/13	1/4	1/4
	TTGV92-42(R2)	18	17/18	17/18	*	*
	untransformed	18	*	*	0/20	0/20
	DLM16 (R1)	18	0/13	0/13	0/5	0/5
	DLM18 (R1)	18	2/16	2/16	0/2	0/2



Table 5, cont.

	Line (Generation)	Days Post Inoculation observation	Fraction of symptom-free and virus-free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
	DLM21 (R1)	18	0/18	0/18	*	*
	DLM24 (R1)	18	1/11	1/11	0/7	0/7
	DLM25 (R1)	18	7/16	6/16	0/2	0/2
	DLM32 (R1)	18	1/16	1/16	0/2	0/2
5	untransformed	18	*	*	0/13	0/13
	DLM39 (R1)	30	0/15	1/15	1/4	1/4
	DLM46 (R1)	18	0/15	0/15	0/5	0/5
	DLM47 (R1)	18	5/17	4/17	0/3	0/3
	DLM48 (R1)	18	0/15	0/15	0/5	0/5
10	DLM49 (R1)	18	1/16	9/16	0/4	0/4
	DLM55 (R1)	18	0/14	0/14	0/6	0/6
	DLM58 (R1)	18	0/14	1/14	0/6	0/6
15	untransformed	30	*	*	0/9	0/9

Table 6. ToMoV Agroinoculations: 3AA Transgenics

	Line (Generation)	DPI observation	Fraction of symptom and virus free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
5	3AA3 (R1)	25	1/14	1/14	0/6	0/6
	3AA7 (R1)	25	3/18	3/18	0/2	0/2
	3AA9 (R1)	25	1/19	1/19	0/1	0/1
	3AA12 (R1)	25	0/14	0/14	0/6	0/6
10	3AA13 (R1)	25	1/4	0/4	0/4	0/4
	3AA16 (R1)	25	1/11	1/11	0/9	0/9
	3AA18 (R1)	25	0/4	0/4	2/20	2/20
	untransformed	25	*	*	0/15	0/15
15	3AA13 (R1)	22	2/19	2/19	0/1	0/1
	3AA21 (R1)	25	3/13	3/13	0/7	0/7
	3AA22 (R1)	22	6/16	9/16	0/4	0/4
	3AA23 (R1)	25	3/9	4/9	0/1	0/1
20	3AA26 (R1)	25	0/16	0/16	0/4	0/4
	3AA27 (R1)	25	0/10	0/10	0/4	0/4
	3AA30 (R1)	25	2/18	5/18	0/2	0/2
	untransformed	25	*	*	0/15	0/15

Table 7. ToMoV Agroinoculations: LAS Transgenics

	Line (Generation)	DPI observation	Fraction of symptom and virus free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
25	LAS6 (R1)	25	8/11	8/11	0/9	0/9
	LAS1 (R1)	25	0/10	0/10	0/10	0/10
	LAS10 (R1)	25	1/14	1/14	1/6	1/6
	LAS11 (R1)	25	*	*	0/20	0/20
30	untransformed	25	*	*	0/14	0/14

Table 8. ToM V Agroinoculations: CODLM Transgenics

	Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
5	CODLM2 (R1)	20	0/14	0/14	0/6	0/6
	CODLM5 (R1)	"	0/15	0/15	0/5	0/5
10	CODLM6 (R1)	"	9/14	3/14	0/6	0/6
	CODLM8 (R1)	"	8/20	1/20	No NPTII- plants	*
	CODLM9 (R1)	"	0/18	0/18	0/2	0/2
15	CODLM10 (R1)	"	0/17	0/17	0/3	0/3
	CODLM13 (R1)	"	11/20	0/20	No NPTII- plants	*
20	CODLM14 (R1)	"	7/16	0/16	0/4	0/4
	untransformed	"	*	*	1/9	1/9

Table 9. ToMoV Agroinoculations: MUA and MUB Transgenics

	Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
5	MUA9	22	8/14	10/14	0/6	0/6
	MUB20	*	10/20	1/20	No NPTII*	*
	MUB37	*	1/14	0/14	0/6	0/6
	MUB3	20	0/14	0/14	0/6	0/6
10	MUB5	*	1/7	0/17	0/3	0/3
	MUB7	*	1/18	1/18	0/2	0/2
	MUA8	*	6/6	5/6	0/14	0/14
	MUA12	*	No NPTII*	*	0/20	0/20
15	MUB14	*	2/15	1/15	0/5	0/5
	MUB15	*	5/20	3/20	No NPTII*	*
	MUA16	*	5/14	4/14	0/6	0/6
	MUA18	22	*	6/6	*	0/14
20	MUB19	*	*	1/11	*	No NPTII*
	MUB26	*	*	0/15	*	0/5
	MUA22	21	*	11/11	*	0/9
	MUB33	*	*	0/15	*	0/5
25	MUB30	*	*	4/12	*	0/8
	MUA28	*	*	12/12	*	0/7
	MUA41	*	*	6/9	*	0/11
	MUB36	*	*	1/15	*	0/5
30	MUA39	*	*	5/14	*	4/6
	MUB31	*	*	2/16	*	0/4
	MUB34	*	*	NO NPTII*	*	0/20
	MUB32	*	*	3/16	*	0/4
	untransformed	*	*	*	0/10	0/10

Tabl 10. ToM V Agroinoculations: RTFS Transg nics

	Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants			
			NPTII positives		NPTII negatives	
			visual	blot	visual	blot
5	RTFS1	20	5/12	2/12	0/8	0/8
	RTFS3	"	0/15	0/15	0/5	0/5
	RTFS4	"	5/16	1/16	0/4	0/4
	RTFS6	"	10/12	10/12	0/8	0/8
	RTFS9	"	5/13	3/13	0/7	0/7
10	RTFS10	"	No NPTII*	*	0/20	0/20
	untransformed	"	*	*	0/10	0/10

#### Example 10.4 Squash Blot Assay of Geminivirus

15 Approximately 3 weeks after agroinoculation, visible symptoms were monitored and compared to untransformed tomato lines. At the same time, two samples per plant of leaf extract were applied to a hybridization membrane. This was done by squashing a leaf disc about  
20 1/8 inch diameter on the membrane such that leaf sap thoroughly impregnated the membrane. After the membrane was treated to denature the DNA in the extract, it was hybridized according to the same  
25 protocol as used for Northern blots with a radioactive probe that would detect the DNA-B component of ToMoV or the C1 ORF of TYLCV. The presence of viral DNA in the plant sap could be detected by autoradiography.

The presence of viral DNA was highly correlated with  
30 appearance of symptoms, an indicia of susceptibility to infection. The virus-free phenotype was correlated with the presence of the marker in families of transgenic tomatoes segregating the NPTII marker.

35 Figure 1 shows that expression of the ToMoV AC1d1m transgene is required for resistance to ToMoV infection

mediated by agroinoculation. High expression is necessary but in itself does not ensure resistance.

#### Example 10.4 Viruliferous Whitefly Inoculations

5 Ten whiteflies carrying ToMoV were put on each eight-day old seedling. Twenty-five seedlings were used per family. In those families of seedlings which were not homozygous for the transgene, NPTII assays were correlated with squash blot results. Twenty-one to  
10 thirty-one days after inoculation, samples of each plant were taken for biochemical and molecular hybridization assays. The results are summarized in Table 11. The Visual Rating gives the average of are plants, in which "0" is no symptoms and "4" is with  
15 most marked symptoms. The squash blot results give the fraction of the plants that were virus free.

Table 11. Florida Greenhouse Whitefly ToMoV Inoculations

Line (Generation)	DPI observation	Fraction of symptom- and virus-free plants		Visual Ratings	Squash Blot Results
		NPTII Positives Blot	NPTII Negatives Blot		
		Blot	Blot		
TGM44 (R2)	21	7/20	0/6	2.2	13/26
TGM44 (R2)	21	6/17	0/9	1.6	10/26
untransformed	21	*	7/25	3.6	7/25
DLM12 (R2)	31	10/26	*	1.0	20/26
DLM12 (R2)	31	8/26	*	2.0	18/26
untransformed	31	*	1/19	3.7	3/19
DLM12 (R2)	31	8/20	*	0.8	8/20
DLM14 (R2)	31	3/11	*	1.7	3/11
DLM14 (R2)	31	9/23	*	3.0	12/23
untransformed	31	*	0/16	2.9	0/16
TTGV92-42 (R2)	32	7/21	1/5	2.5	23/26
TTGV92-42 (R3)	32	22/26	*	0	26/26
untransf.	32	*	*	3.8	6/15
XPH5978	32	*	10/26	2.9	No Data
XPH5979	32	*	7/26	2.7	No Data

## Example 11. Transdominance in plant cell lines

A mutated form of AC1 protein of BGMV inhibits replication of DNA-A in a tobacco suspension cell system. To evaluate AC1 protein mutants for their potential to interfere with viral replication, a transient assay was used to detect trans-dominant interference activity of the mutant viral ORF. (Table 12 and Fig. 2.).

**Table 12. Effects of BGMV AC1 Mutations on Replication and Transdominance**

5		Mutation	Replication	Trans-dominance
		WT AC1	+	0%
		mutation 1(a)	-	90%
		mutation 1(c)	-	90%
		I <sup>100</sup> R	+	0%
10		mutation 2(c)	+	0%
		mutation 2(a)	-	50-80%
		mutation 3(a)	-	>95%
		mutations 2(a) and (c)	-	50-80%

15 NT-1 cells were inoculated with wildtype DNA-A or a lethal mutant of DNA-A of BGMV-GA (ADM; double mutations 2(a) and (c) in combination with carrier DNA (PBS) or AC1 transexpression vectors containing mutated forms of AC1 ORF. Total DNA was harvested from the

20 NT-1 tobacco cells at 72 hours after inoculation, electrophoresed in an agarose gel, blotted onto paper and probed with a radiolabeled DNA probe corresponding to the coat protein of BGMV-GA DNA-A. The results demonstrate that wildtype AC1 protein produced in trans

25 can replicate a lethal AC1 mutant of DNA-A. More importantly, the results show that codon changes in the nicking motif of the AC1 ORF abolished infectivity and replication. In the transient assay for trans-dominance interference, double mutations 1(a) and

30 1(c) showed trans-dominance interference (Table 12).

Additional experimental treatments included:

35 A+PBS: wildtype BGMV-DNA-A was introduced into NT-1 cells with PBS at DNA weight ratios of 1:100 and 5:95 wildtype:PBS;



A+TDM: BGMV-DNA-A was introduced into NT-1 cells with transexpression vector coding for double mutations 2(a) and 2(c) at ratios of 1:100 and 5:95;

5

A+TD<sup>262</sup>R: BGMV-DNA-A was introduced with transexpression vector coding for mutation 3(a) at ratios of 1:100 and 5:95;

10 ADM+PBS: DNA-A containing double mutations 2(a) and 2(c) with PBS at 5:95;

ADM+TAC1: DNA-A containing double mutations 2(a) and 2(c) with transexpression vector coding for  
15 wildtype AC1 at a ratio of 5:95.

The transexpression vectors used in these experiments express AC1 in the proper context for replication.

20 Figure 1 represents the results of these experiments. The mutations created in the 35S promoter driven AC1 ORF are listed in the first column. These ORF are used in trans with wild-type DNA-A of BGMV-GA to determine transdominance interference. Replication was tested in  
25 an NT-1 cell system. Replication is presented as the amount of reduction in replication in comparison to wild-type replication level. Trans-dominance was determined by engineering each mutation into a AC1 transexpression vectors which contained the AC1 ORF  
30 under control of the CaMV 35S promoter. Mutant AC1 expression vectors were coinoculated into NT-1 cells along with WT DNA-A and reductions in DNA-A replication were estimated from autoradiograms. Trans-dominance data are expressed as the observed reduction in DNA-A  
35 replication when co-inoculated with each AC1 mutant. Mutation 2(c) confers a temperature sensitive phenotype

for replication, supporting replication at 23°C but not at 28°C.

- Replication was observed in inoculations with wildtype BGMV-DNA-A plus carrier DNA (A+PBS) (Fig. 1). No replication was observed in inoculations with a mutant of DNA-A containing double mutations 2(a) and 2(c) coinoculated with carrier DNA (ADM+PBS). Replication of double mutations 2(a) and 2(c) was, however, complemented by transexpression of wildtype AC1 in the transient expression vector (ADM+TAC1). Replication of BGMV-DNA-A in the presence of two different AC1 mutants, treatments A+TDM and A+TD<sup>262</sup>R reduced replication of virus DNA-A compared to the A+PBS treatments. Accordingly, transexpression of AC1 mutants can inhibit replication of BGMV-DNA-A. Further lethal mutants of AC1 inhibit replication when expressed in trans to DNA-A.
- The results show that non-lethal mutants do not exhibit detectable transdominant activity. While levels of transdominance varied among different AC1 mutants, only replication-lethal mutants exhibited transdominant interference. Levels of AC1 expression directly relate to levels of trans-dominance and replication (Fig. 1). Thus, AC1 expression, results in production of a protein that mediates the "trans"-effective suppression. That is, this protein likely binds to the CR region which mediates its suppressive effect by inhibiting the binding of the wildtype AC1 protein.

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(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Mottle Gemini Virus  
(C) INDIVIDUAL ISOLATE: Florida

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 44..1130

## (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Gilbertson, RL  
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(B) TITLE: Pseudorecombination between the infectious  
cloned DNA components of tomato mottle and bean  
dwarf mosaic geminiviruses.  
(C) JOURNAL: Jour. General Virol.  
(D) VOLUME: 74  
(F) PAGES: 23-31  
(G) DATE: 1993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG	103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln	
5 10 15 20	
TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT	151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn	
25 30 35	
ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA	199
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu	
40 45 50	
AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC	247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr	
55 60 65	
CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA	295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser	
70 75 80	
GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC	343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val	
85 90 95 100	
AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC	391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe	
105 110 115	
CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT	439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp	

	120		125		130												
TCA Ser	TAT Tyr	GCG Ala	AAA Lys	GCG Ala	TTA Leu	AAT Asn	GCA Ala	AGT Ser	TCG Ser	GTT Val	CAA Gln	TCT Ser	GCC Ala	TTA Leu	GCA Ala	487	
						135	140										
GTT Val	CTA Leu	AGG Arg	GAA Glu	GAA Glu	CAA Gln	CCA Pro	AAA Lys	GAT Asp	TTT Phe	GTA Val	TTA Leu	CAA Gln	AAT Asn	CAT His	AAC Asn	535	
						150	155										
ATC Ile	CGC Arg	TCT Ser	AAC Asn	CTA Leu	GAA Glu	CGA Arg	ATA Ile	TTC Phe	GCA Ala	AAG Lys	GCT Ala	CCG Pro	GAA Glu	CCG Pro	TGG Trp	583	
						165	170	175								180	
GTT Val	CCT Pro	CCA Pro	TTT Phe	CAA Gln	GTC Val	TCT Ser	TCT Ser	TTC Phe	ACT Thr	AAC Asn	GTT Val	CCT Pro	GAC Asp	GAG Glu	ATG Met	631	
						185										190	195
CAG Gln	GAA Glu	TGG Trp	GCG Ala	GAT Asp	AAT Asn	TAT Tyr	TTC Phe	GGG Gly	ACG Thr	GGT Gly	GCA Ala	GCT Ala	GCG Ala	CCG Arg	CCA Pro	679	
						200	205										210
GAG Glu	AGA Arg	CCT Pro	GTA Val	AGT Ser	ATC Ile	ATC Ile	GTC Val	GAG Glu	GGT Gly	GAT Asp	TCA Ser	AGA Arg	ACA Thr	GGG Gly	AAG Lys	727	
						215	220										225
ACG Thr	ATG Met	TGG Trp	GCA Ala	CGT Arg	GCG Ala	TTA Leu	GGC Gly	CCA Pro	CAT His	AAC Asn	TAT Tyr	CTC Leu	AGT Ser	GGA Gly	CAC His	775	
						230	235										240
CTA Leu	GAC Asp	TTC Phe	AAT Asn	GGT Gly	CGA Arg	GTC Val	TTC Phe	TCG Ser	AAT Asn	GAT Asp	GTG Val	CAG Gln	TAT Tyr	AAC Asn	GTC Val	823	
						245	250	255								260	
ATT Ile	GAT Asp	GAC Asp	ATC Ile	GCA Ala	CCG Pro	CAT His	TAT Tyr	CTA Leu	AAG Lys	CTA Leu	AAG Lys	CAC His	TGG Trp	AAA Lys	GAA Glu	871	
						265	270										275
TTG Leu	CTA Leu	GGG Gly	GCC Ala	CAG Gln	AAA Lys	GAT Asp	TGG Trp	CAA Gln	TCA Ser	AAT Asn	TGC Cys	AAG Lys	TAC Tyr	GGT Gly	AAG Lys	919	
						280	285										290
CCA Pro	GTT Val	CAA Gln	ATT Ile	AAA Lys	GGC Gly	GGA Gly	ATC Ile	CCA Pro	GCA Ala	ATC Ile	GTG Val	CTT Leu	TGC Cys	AAT Asn	CCT Pro	967	
						295	300										305
GGT Gly	GAG Glu	GGT Gly	GCC Ala	AGC Ser	TAT Tyr	AAA Lys	GAG Glu	TTC Phe	TTA Leu	GAC Asp	AAA Lys	GCA Ala	GAA Glu	AAT Asn	ACA Thr	1015	
						310	315	320									
GGT Gly	CTA Leu	AAG Lys	AAC Asn	TGG Trp	ACT Thr	GTC Val	AAG Lys	AAT Asn	GCG Ala	ATC Ile	TTC Phe	ATC Ile	ACC Thr	CTC Leu	ACA Thr	1063	
						325	330	335								340	
GCC Ala	CCC Pro	CTC Leu	TAT Tyr	CAA Gln	GAC Asp	AGC Ser	ACA Thr	CAG Gln	GCA Ala	AGC Ser	CAA Gln	GAA Glu	ACG Thr	GGC Gly	AAT Asn	1111	
						345										350	355
CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCTA																1160	
Gln Lys Ala Gln Gly *																	

362

GG

1162

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Thr	Tyr	Pro	Gln	Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ala	Leu	Ser	Gln	Leu	20	25	30	
Gln	Asn	Leu	Asn	Thr	Pro	Val	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	Arg	35	40	45	
Glu	Leu	His	Glu	Asn	Gly	Glu	Pro	His	Leu	His	Val	Leu	Val	Gln	Phe	50	55	60	
Glu	Gly	Lys	Tyr	Gln	Cys	Thr	Asn	Asn	Arg	Phe	Phe	Asp	Leu	Val	Ser	65	70	75	80
Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Gly	Ala	Lys	Ser	85	90	95	
Ser	Ser	Asp	Val	Lys	Ser	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Ile	Glu	100	105	110	
Trp	Gly	Asp	Phe	Gln	Ile	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Gln	Gln	115	120	125	
Ser	Ala	Asn	Asp	Ser	Tyr	Ala	Lys	Ala	Leu	Asn	Ala	Ser	Ser	Val	Gln	130	135	140	
Ser	Ala	Leu	Ala	Val	Leu	Arg	Glu	Glu	Gln	Pro	Lys	Asp	Phe	Val	Leu	145	150	155	160
Gln	Asn	His	Asn	Ile	Arg	Ser	Asn	Leu	Glu	Arg	Ile	Phe	Ala	Lys	Ala	165	170	175	
Pro	Glu	Pro	Trp	Val	Pro	Pro	Phe	Gln	Val	Ser	Ser	Phe	Thr	Asn	Val	180	185	190	
Pro	Asp	Glu	Met	Gln	Glu	Trp	Ala	Asp	Asn	Tyr	Phe	Gly	Thr	Gly	Ala	195	200	205	
Ala	Ala	Arg	Pro	Glu	Arg	Pro	Val	Ser	Ile	Ile	Val	Glu	Gly	Asp	Ser	210	215	220	
Arg	Thr	Gly	Lys	Met	Trp	Ala	Arg	Ala	Leu	Gly	Pro	His	Asn	Tyr		225	230	235	240

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 1169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

1) (ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

55

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Lys	Lys	Phe	Arg	Val	Gln	Ser	Lys	Asn	Tyr	Phe	Leu	Thr	Tyr	Pro	Gln				
			370					375					380						
TGC	TCT	TTG	TCT	AAA	GAA	GAA	GCA	CTT	TCC	CAA	TTA	CAA	AAC	CTA	AAT				151
Cys	Ser	Leu	Ser	Lys	Glu	Glu	Ala	Leu	Ser	Gln	Leu	Gln	Asn	Leu	Asn				
		385					390					395							
ACC	CCA	GTC	AAT	AAG	AAA	TTC	ATC	AAA	ATT	TGC	AGA	GAG	CTT	CAT	GAA				199
Thr	Pro	Val	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	Arg	Glu	Leu	His	Glu				
	400					405					410								
AAT	GGG	GAA	CCT	CAT	CTC	CAT	GTG	CTT	GTT	CAG	TTC	GAA	GGA	AAG	TAC				247
Asn	Gly	Glu	Pro	His	Leu	His	Val	Leu	Val	Gln	Phe	Glu	Gly	Lys	Tyr				
415					420					425					430				
CAG	TGC	ACG	AAT	AAC	AGA	TTC	TTC	GAC	CTG	GTC	TCC	CCA	ACC	CGG	TCA				295
Gln	Cys	Thr	Asn	Asn	Arg	Phe	Phe	Asp	Leu	Val	Ser	Pro	Thr	Arg	Ser				
			435					440						445					
GCA	CAT	TTC	CAT	CCG	AAT	ATT	CAG	GGA	GCT	AAA	TCG	AGC	TCC	GAC	GTC				343
Ala	His	Phe	His	Pro	Asn	Ile	Gln	Gly	Ala	Lys	Ser	Ser	Ser	Asp	Val				
			450				455					460							
AAA	TCG	TAC	ATC	GAC	AAG	GAC	GGA	GAT	ACA	ATC	GAA	TGG	GGA	GAT	TTC				391
Lys	Ser	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Ile	Glu	Trp	Gly	Asp	Phe				
	465					470					475								
CAG	ATC	GAC	GGC	AGA	TCT	GCC	AGA	GGA	GGC	CAG	CAG	TCT	GCT	AAT	GAT				439
Gln	Ile	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Gln	Gln	Ser	Ala	Asn	Asp				
	480					485					490								
TCA	TAT	GCG	AAA	GCG	TTA	AAT	GCA	AGT	TCG	GTT	CAA	TCT	GCC	TTA	GCA				487
Ser	Tyr	Ala	Lys	Ala	Leu	Asn	Ala	Ser	Ser	Val	Gln	Ser	Ala	Leu	Ala				
495					500					505				510					
GTT	CTA	AGG	GAA	GAA	CAA	CCA	AAA	GAT	TTT	GTA	TTA	CAA	AAT	CAT	AAC				535
Val	Leu	Arg	Glu	Glu	Gln	Pro	Lys	Asp	Phe	Val	Leu	Gln	Asn	His	Asn				
			515					520				525							
ATC	CGC	TCT	AAC	CTA	GAA	CGA	ATA	TTC	GCA	AAG	GCT	CCG	GAA	CCG	TGG				583
Ile	Arg	Ser	Asn	Leu	Glu	Arg	Ile	Phe	Ala	Lys	Ala	Pro	Glu	Pro	Trp				
			530				535					540							
GTT	CCT	CCA	TTT	CAA	GTC	TCT	TCT	TTC	ACT	AAC	GTT	CCT	GAC	GAG	ATG				631
Val	Pro	Pro	Phe	Gln	Val	Ser	Ser	Phe	Thr	Asn	Val	Pro	Asp	Glu	Met				
	545					550						555							
CAG	GAA	TGG	GCG	GAT	AAT	TAT	TTC	GGG	ACG	GGT	GCA	GCT	GCG	CGG	CCA				679
Gln	Glu	Trp	Ala	Asp	Asn	Tyr	Phe	Gly	Thr	Gly	Ala	Ala	Ala	Arg	Pro				
	560				565						570								
GAG	AGA	CCT	GTA	AGT	ATC	ATC	GTC	GAG	GGT	GAT	TCA	AGA	ACA	GGG	CAC				727
Glu	Arg	Pro	Val	Ser	Ile	Ile	Val	Glu	Gly	Asp	Ser	Arg	Thr	Gly	His				
575				580				585						590					
ACG	ATG	TGG	GCA	CGT	GCG	TTA	GGC	CCA	CAT	AAC	TAT	CTC	AGT	GGA	CAC				775



Thr	Met	Trp	Ala	Arg	Ala	Leu	Gly	Pro	His	Asn	Tyr	Leu	Ser	Gly	His	
				595					600					605		
CTA	GAC	TTC	AAT	GGT	CGA	GTC	TTC	TCG	AAT	GAT	GTG	CAG	TAT	AAC	GTC	323
Leu	Asp	Phe	Asn	Gly	Arg	Val	Phe	Ser	Asn	Asp	Val	Gln	Tyr	Asn	Val	
			610					615				620				
ATT	AAA	TAC	ATC	GCA	CCG	CAT	TAT	CTA	AAG	CTA	AAG	CAC	TGG	AAA	GAA	871
Ile	Lys	Tyr	Ile	Ala	Pro	His	Tyr	Leu	Lys	Leu	Lys	His	Trp	Lys	Glu	
		625					630					635				
TTG	CTA	GGG	GCC	CAG	AAA	GAT	TGG	CAA	TCA	AAT	TGC	AAG	TAC	GGT	AAG	919
Leu	Leu	Gly	Ala	Gln	Lys	Asp	Trp	Gln	Ser	Asn	Cys	Lys	Tyr	Gly	Lys	
	640					645					650					
CCA	GTT	CAA	ATT	AAA	GGC	GGA	ATC	CCA	GCA	ATC	GTG	CTT	TGC	AAT	CCT	967
Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ala	Ile	Val	Leu	Cys	Asn	Pro	
655					660					665					670	
GGT	GAG	GGT	GCC	AGC	TAT	AAA	GAG	TTC	TTA	GAC	AAA	GCA	GAA	AAT	ACA	1015
Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Glu	Phe	Leu	Asp	Lys	Ala	Glu	Asn	Thr	
			675					680						685		
GGT	CTA	AAG	AAC	TGG	ACT	GTC	AAG	AAT	GCG	ATC	TTC	ATC	ACC	CTC	ACA	1063
Gly	Leu	Lys	Asn	Trp	Thr	Val	Lys	Asn	Ala	Ile	Phe	Ile	Thr	Leu	Thr	
			690					695					700			
GCC	CCC	CTC	TAT	CAA	GAC	AGC	ACA	CAG	GCA	AGC	CAA	GAA	ACG	GGC	AAT	1111
Ala	Pro	Leu	Tyr	Gln	Asp	Ser	Thr	Gln	Ala	Ser	Gln	Glu	Thr	Gly	Asn	
		705					710					715				
CAG	AAG	GCG	CAG	GGT	TGA	T	CTACAGT	GCG	GGTGCTCCAT	CTACTTCCAC						1160
Gln	Lys	Ala	Gln	Gly	*											
		720														
TTAGACTGT																1169

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15

Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu  
 20 25 30

Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg  
 35 40 45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe  
 50 55 60

51u Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu  
 100 105 110  
 Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln  
 130 135 140  
 Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu  
 145 150 155 160  
 Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala  
 165 170 175  
 Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val  
 180 185 190  
 Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala  
 195 200 205  
 Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser  
 210 215 220  
 Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr  
 225 230 235 240  
 Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val  
 245 250 255  
 Gln Tyr Asn Val Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys  
 260 265 270  
 His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys  
 275 280 285  
 Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val  
 290 295 300  
 Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys  
 305 310 315 320  
 Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe  
 325 330 335  
 Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln  
 340 345 350  
 Glu Thr Gly Asn Gln Lys Ala Gln Gly \*  
 355 360

(2) INFORMATION FOR SEQ ID NO:5:

## 1. SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Mottle Gemini Virus
- (B) STRAIN: Florida

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 44..1130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA	55
Met Pro Pro Pro	
365	
AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG	103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln	
370 375 380	
TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT	151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn	
385 390 395	
ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA	199
Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg Glu Leu His Glu	
400 405 410	
AAT GGG GAA CCT CAT CTC CAT GTG CTT GTT CAG TTC GAA GGA AAG TAC	247
Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe Glu Gly Lys Tyr	
415 420 425 430	
CAG TGC ACG AAT AAC AGA TTC TTC GAC CTG GTC TCC CCA ACC CGG TCA	295
Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser Pro Thr Arg Ser	
435 440 445	
GCA CAT TTC CAT CCG AAT ATT CAG GGA GCT AAA TCG AGC TCC GAC GTC	343
Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser Asp Val	
450 455 460	
AAA TCG TAC ATC GAC AAG GAC GGA GAT ACA ATC GAA TGG GGA GAT TTC	391
Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu Trp Gly Asp Phe	
465 470 475	
CAG ATC GAC GGC AGA TCT GCC AGA GGA GGC CAG CAG TCT GCT AAT GAT	439
Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp	
480 485 490	
TCA TAT GCG AAA GCG TTA AAT GCA AGT TCG GTT CAA TCT GCC TTA GCA	487

Ser 495	Tyr	Ala	Lys	Ala	Leu 500	Asn	Ala	Ser	Ser	Val 505	Gln	Ser	Ala	Leu	Ala 510	
GTT	CTA	AGG	GAA	GAA	CAA	CCA	AAA	GAT	TTT	GTA	TTA	CAA	AAT	CAT	AAC	535
Val	Leu	Arg	Glu	Glu	Gln	Pro	Lys	Asp	Phe	Val	Leu	Gln	Asn	His	Asn	
				515					520					525		
ATC	CGC	TCT	AAC	CTA	GAA	CGA	ATA	TTC	GCA	AAG	GCT	CCG	GAA	CCG	TGG	583
Ile	Arg	Ser	Asn	Leu	Glu	Arg	Ile	Phe	Ala	Lys	Ala	Pro	Glu	Pro	Trp	
			530					535					540			
GTT	CCT	CCA	TTT	CAA	GTC	TCT	TCT	TTC	ACT	AAC	GTT	CCT	GAC	GAG	ATG	631
Val	Pro	Pro	Phe	Gln	Val	Ser	Ser	Phe	Thr	Asn	Val	Pro	Asp	Glu	Met	
		545					550					555				
CAG	GAA	TGG	GCG	GAT	AAT	TAT	TTC	GGG	ACG	GGT	GCA	GCT	GCG	CGG	CCA	679
Gln	Glu	Trp	Ala	Asp	Asn	Tyr	Phe	Gly	Thr	Gly	Ala	Ala	Ala	Arg	Pro	
	560					565					570					
GAG	AGA	CCT	GTA	AGT	ATC	ATC	GTC	GAG	GGT	GAT	TCA	AGA	ACA	GGG	CAC	727
Glu	Arg	Pro	Val	Ser	Ile	Ile	Val	Glu	Gly	Asp	Ser	Arg	Thr	Gly	His	
575					580					585					590	
ACG	ATG	TGG	GCA	CGT	GCG	TTA	GGC	CCA	CAT	AAC	TAT	CTC	AGT	GGA	CAC	775
Thr	Met	Trp	Ala	Arg	Ala	Leu	Gly	Pro	His	Asn	Tyr	Leu	Ser	Gly	His	
				595					600					605		
CTA	GAC	TTC	AAT	GGT	CGA	GTC	TTC	TCG	AAT	GAT	GTG	CAG	TAT	AAC	GTC	823
Leu	Asp	Phe	Asn	Gly	Arg	Val	Phe	Ser	Asn	Asp	Val	Gln	Tyr	Asn	Val	
			610					615					620			
ATT	GAT	GAC	ATC	GCA	CCG	CAT	TAT	CTA	AAG	CTA	AAG	CAC	TGG	AAA	GAA	871
Ile	Asp	Asp	Ile	Ala	Pro	His	Tyr	Leu	Lys	Leu	Lys	His	Trp	Lys	Glu	
		625					630					635				
TTG	CTA	GGG	GCC	CAG	AAA	GAT	TGG	CAA	TCA	AAT	TGC	AAG	TAC	GGT	AAG	919
Leu	Leu	Gly	Ala	Gln	Lys	Asp	Trp	Gln	Ser	Asn	Cys	Lys	Tyr	Gly	Lys	
	640					645					650					
CCA	GTT	CAA	ATT	AAA	GGC	GGA	ATC	CCA	GCA	ATC	GTG	CTT	TGC	AAT	CCT	967
Pro	Val	Gln	Ile	Lys	Gly	Gly	Ile	Pro	Ala	Ile	Val	Leu	Cys	Asn	Pro	
655					660					665					670	
GGT	GAG	GGT	GCC	AGC	TAT	AAA	GAG	TTC	TTA	GAC	AAA	GCA	GAA	AAT	ACA	1015
Gly	Glu	Gly	Ala	Ser	Tyr	Lys	Glu	Phe	Leu	Asp	Lys	Ala	Glu	Asn	Thr	
				675					680					685		
GGT	CTA	AAG	AAC	TGG	ACT	GTC	AAG	AAT	GCG	ATC	TTC	ATC	ACC	CTC	ACA	1063
Gly	Leu	Lys	Asn	Trp	Thr	Val	Lys	Asn	Ala	Ile	Phe	Ile	Thr	Leu	Thr	
			690					695					700			
GCC	CCC	CTC	TAT	CAA	GAC	AGC	ACA	CAG	GCA	AGC	CAA	GAA	ACG	GGC	AAT	1111
Ala	Pro	Leu	Tyr	Gln	Asp	Ser	Thr	Gln	Ala	Ser	Gln	Glu	Thr	Gly	Asn	
		705					710					715				
CAG	AAG	GCG	CAG	GGT	TGA	T	CTACAGT	GCG	GGTGCTCCAT	CTACTTCCAC						1160
Gln	Lys	Ala	Gln	Gly	*											
	720															
TTAGACTGT																1169

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met  Pro  Pro  Pro  Lys  Lys  Phe  Arg  Val  Gln  Ser  Lys  Asn  Tyr  Phe  Leu
 1              5              10              15

Thr  Tyr  Pro  Gln  Cys  Ser  Leu  Ser  Lys  Glu  Glu  Ala  Leu  Ser  Gln  Leu
              20              25              30

Gln  Asn  Leu  Asn  Thr  Pro  Val  Asn  Lys  Lys  Phe  Ile  Lys  Ile  Cys  Arg
              35              40              45

Glu  Leu  His  Glu  Asn  Gly  Glu  Pro  His  Leu  His  Val  Leu  Val  Gln  Phe
 50              55              60

Glu  Gly  Lys  Tyr  Gln  Cys  Thr  Asn  Asn  Arg  Phe  Phe  Asp  Leu  Val  Ser
 65              70              75              80

Pro  Thr  Arg  Ser  Ala  His  Phe  His  Pro  Asn  Ile  Gln  Gly  Ala  Lys  Ser
              85              90              95

Ser  Ser  Asp  Val  Lys  Ser  Tyr  Ile  Asp  Lys  Asp  Gly  Asp  Thr  Ile  Glu
 100              105              110

Trp  Gly  Asp  Phe  Gln  Ile  Asp  Gly  Arg  Ser  Ala  Arg  Gly  Gly  Gln  Gln
 115              120              125

Ser  Ala  Asn  Asp  Ser  Tyr  Ala  Lys  Ala  Leu  Asn  Ala  Ser  Ser  Val  Gln
 130              135              140

Ser  Ala  Leu  Ala  Val  Leu  Arg  Glu  Glu  Gln  Pro  Lys  Asp  Phe  Val  Leu
 145              150              155              160

Gln  Asn  His  Asn  Ile  Arg  Ser  Asn  Leu  Glu  Arg  Ile  Phe  Ala  Lys  Ala
              165              170              175

Pro  Glu  Pro  Trp  Val  Pro  Pro  Phe  Gln  Val  Ser  Ser  Phe  Thr  Asn  Val
              180              185              190

Pro  Asp  Glu  Met  Gln  Glu  Trp  Ala  Asp  Asn  Tyr  Phe  Gly  Thr  Gly  Ala
 195              200              205

Ala  Ala  Arg  Pro  Glu  Arg  Pro  Val  Ser  Ile  Ile  Val  Glu  Gly  Asp  Ser
 210              215              220

Arg  Thr  Gly  His  Thr  Met  Trp  Ala  Arg  Ala  Leu  Gly  Pro  His  Asn  Tyr
 225              230              235              240

Leu  Ser  Gly  His  Leu  Asp  Phe  Asn  Gly  Arg  Val  Phe  Ser  Asn  Asp  Val
              245              250              255

```

Gln Tyr Asn Val Ile Asp Asp Ile Ala Pro His Tyr Leu Lys Leu Lys  
 250 265 270

His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys  
 275 280 285

Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val  
 290 295 300

Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys  
 305 310 315 320

Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe  
 325 330 335

Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln  
 340 345 350

Glu Thr Gly Asn Gln Lys Ala Gln Gly \*

355 360

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1169 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Tomato Mottle Gemini Virus
  - (B) STRAIN: Florida
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 44..1130

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA	55
Met Pro Pro Pro	365
AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG	103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln	370 375 380
TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT	151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn	385 390 395
ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA	199

Thr	Pro	Val	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Cys	Arg	Glu	Leu	His	Glu	
400						405				410						
AAT	GGG	GAA	CCT	CAT	CTC	CAT	GTG	CTT	GTT	CAG	TTC	GAA	GGA	AAG	TAC	247
Asn	Gly	Glu	Pro	His	Leu	His	Val	Leu	Val	Gln	Phe	Glu	Gly	Lys	Tyr	
415					420					425					430	
CAG	TGC	ACG	AAT	AAC	AGA	TTC	TTC	GAC	CTG	GTC	TCC	CCA	ACC	CGG	TCA	295
Gln	Cys	Thr	Asn	Asn	Arg	Phe	Phe	Asp	Leu	Val	Ser	Pro	Thr	Arg	Ser	
				435					440					445		
GCA	CAT	TTC	CAT	CCG	AAT	ATT	CAG	GGA	GCT	AAA	TCG	AGC	TCC	GAC	GTC	343
Ala	His	Phe	His	Pro	Asn	Ile	Gln	Gly	Ala	Lys	Ser	Ser	Ser	Asp	Val	
			450					455					460			
AAA	TCG	TAC	ATC	GAC	AAG	GAC	GGA	GAT	ACA	ATC	GAA	TGG	GGA	GAT	TTC	391
Lys	Ser	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Ile	Glu	Trp	Gly	Asp	Phe	
		465					470					475				
CAG	ATC	GAC	GGC	AGA	TCT	GCC	AGA	GGA	GGC	CAG	CAG	TCT	GCT	AAT	GAT	439
Gln	Ile	Asp	Gly	Arg	Ser	Ala	Arg	Gly	Gly	Gln	Gln	Ser	Ala	Asn	Asp	
	480					485					490					
TCA	TAT	GCG	AAA	GCG	TTA	AAT	GCA	AGT	TCG	GTT	CAA	TCT	GCC	TTA	GCA	487
Ser	Tyr	Ala	Lys	Ala	Leu	Asn	Ala	Ser	Ser	Val	Gln	Ser	Ala	Leu	Ala	
495					500					505				510		
GTT	CTA	AGG	GAA	GAA	CAA	CCA	AAA	GAT	TTT	GTA	TTA	CAA	AAT	CAT	AAC	535
Val	Leu	Arg	Glu	Glu	Gln	Pro	Lys	Asp	Phe	Val	Leu	Gln	Asn	His	Asn	
				515					520					525		
ATC	CGC	TCT	AAC	CTA	GAA	CGA	ATA	TTC	GCA	AAG	GCT	CCG	GAA	CCG	TGG	583
Ile	Arg	Ser	Asn	Leu	Glu	Arg	Ile	Phe	Ala	Lys	Ala	Pro	Glu	Pro	Trp	
			530					535					540			
GTT	CCT	CCA	TTT	CAA	GTC	TCT	TCT	TTC	ACT	AAC	GTT	CCT	GAC	GAG	ATG	631
Val	Pro	Pro	Phe	Gln	Val	Ser	Ser	Phe	Thr	Asn	Val	Pro	Asp	Glu	Met	
		545					550					555				
CAG	GAA	TGG	GCG	GAT	AAT	TAT	TTC	GGG	ACG	GGT	GCA	GCT	GCG	CGG	CCA	679
Gln	Glu	Trp	Ala	Asp	Asn	Tyr	Phe	Gly	Thr	Gly	Ala	Ala	Ala	Arg	Pro	
	560					565					570					
GAG	AGA	CCT	GTA	AGT	ATC	ATC	GTC	GAG	GGT	GAT	TCA	AGA	ACA	GGG	AAG	727
Glu	Arg	Pro	Val	Ser	Ile	Ile	Val	Glu	Gly	Asp	Ser	Arg	Thr	Gly	Lys	
575					580					585					590	
ACG	ATG	TGG	GCA	CGT	GCG	TTA	GGC	CCA	CAT	AAC	TAT	CTC	AGT	GGA	CAC	775
Thr	Met	Trp	Ala	Arg	Ala	Leu	Gly	Pro	His	Asn	Tyr	Leu	Ser	Gly	His	
				595					600					605		
CTA	GAC	TTC	AAT	GGT	CGA	GTC	TTC	TCG	AAT	GAT	GTG	CAG	TAT	AAC	GTC	823
Leu	Asp	Phe	Asn	Gly	Arg	Val	Phe	Ser	Asn	Asp	Val	Gln	Tyr	Asn	Val	
			610					615					620			
ATT	AAA	TAC	ATC	GCA	CCG	CAT	TAT	CTA	AAG	CTA	AAG	CAC	TGG	AAA	GAA	871
Ile	Lys	Tyr	Ile	Ala	Pro	His	Tyr	Leu	Lys	Leu	Lys	His	Trp	Lys	Glu	
		625					630					635				
TTG	CTA	GGG	GCC	CAG	AAA	GAT	TGG	CAA	TCA	AAT	TGC	AAG	TAC	GGT	AAG	919

Leu 640 Gly Ala Gln Lys 645 Asp Trp Gln Ser Asn 650 Cys Lys Tyr Gly Lys  
 CCA GTT CAA ATT AAA GGC GGA ATC CCA GCA ATC GTG CTT TGC AAT CCT 967  
 Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val Leu Cys Asn Pro 670  
 655 660 665  
 GGT GAG GGT GCC AGC TAT AAA GAG TTC TTA GAC AAA GCA GAA AAT ACA 1015  
 Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys Ala Glu Asn Thr 685  
 675 680  
 GGT CTA AAG AAC TGG ACT GTC AAG AAT GCG ATC TTC ATC ACC CTC ACA 1063  
 Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe Ile Thr Leu Thr 700  
 690 695  
 GCC CCC CTC TAT CAA GAC AGC ACA CAG GCA AGC CAA GAA ACG GGC AAT 1111  
 Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln Glu Thr Gly Asn 715  
 705 710  
 CAG AAG GCG CAG GGT TGA T CTACAGTGCG GGTGCTCCAT CTACTTCCAC 1160  
 Gln Lys Ala Gln Gly \* 720  
 TTAGACTGT 1169

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Pro Pro Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15  
 Thr Tyr Pro Gln Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu  
 20 25 30  
 Gln Asn Leu Asn Thr Pro Val Asn Lys Lys Phe Ile Lys Ile Cys Arg  
 35 40 45  
 Glu Leu His Glu Asn Gly Glu Pro His Leu His Val Leu Val Gln Phe  
 50 55 60  
 Glu Gly Lys Tyr Gln Cys Thr Asn Asn Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Thr Ile Glu  
 100 105 110  
 Trp Gly Asp Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125



Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Ser Ser Val Gln  
 130 135 140  
 Ser Ala Leu Ala Val Leu Arg Glu Glu Gln Pro Lys Asp Phe Val Leu  
 145 150 155 160  
 Gln Asn His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Ala Lys Ala  
 165 170 175  
 Pro Glu Pro Trp Val Pro Pro Phe Gln Val Ser Ser Phe Thr Asn Val  
 180 185 190  
 Pro Asp Glu Met Gln Glu Trp Ala Asp Asn Tyr Phe Gly Thr Gly Ala  
 195 200 205  
 Ala Ala Arg Pro Glu Arg Pro Val Ser Ile Ile Val Glu Gly Asp Ser  
 210 215 220  
 Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr  
 225 230 235 240  
 Leu Ser Gly His Leu Asp Phe Asn Gly Arg Val Phe Ser Asn Asp Val  
 245 250 255  
 Gln Tyr Asn Val Ile Lys Tyr Ile Ala Pro His Tyr Leu Lys Leu Lys  
 260 265 270  
 His Trp Lys Glu Leu Leu Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys  
 275 280 285  
 Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ala Ile Val  
 290 295 300  
 Leu Cys Asn Pro Gly Glu Gly Ala Ser Tyr Lys Glu Phe Leu Asp Lys  
 305 310 315 320  
 Ala Glu Asn Thr Gly Leu Lys Asn Trp Thr Val Lys Asn Ala Ile Phe  
 325 330 335  
 Ile Thr Leu Thr Ala Pro Leu Tyr Gln Asp Ser Thr Gln Ala Ser Gln  
 340 345 350  
 Glu Thr Gly Asn Gln Lys Ala Gln Gly \*  
 355 360

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## v1. ORIGINAL SOURCE:

(A) ORGANISM: FL2549B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATCGGATCC GAGTAACTCA TCTGGAGTAC C

31

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: FL1108B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TATCGGATCC GGAAGTAGAT GGAGCACCCG C

31

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PFAC1680

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAAGAACAGG GCACACGATG TGGG

24

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PFAC1781

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTATAACGTC ATTAAATACA TCGCACCGC

29

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Mottle Geminivirus
- (C) INDIVIDUAL ISOLATE: Florida

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 44..439

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGAGT AACTCATCTG GAGTACCCCT TCTTATTACA AAA ATG CCC CCA CCA	55
Met Pro Pro Pro	
365	
AAG AAA TTT AGA GTT CAG TCA AAG AAC TAT TTC CTC ACT TAT CCA CAG	103
Lys Lys Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu Thr Tyr Pro Gln	
370 375 380	
TGC TCT TTG TCT AAA GAA GAA GCA CTT TCC CAA TTA CAA AAC CTA AAT	151
Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Gln Asn Leu Asn	
385 390 395	
ACC CCA GTC AAT AAG AAA TTC ATC AAA ATT TGC AGA GAG CTT CAT GAA	199

Thr	Pro	Val	Asn	Lys	Lys	Phe	Ile	Lys	Ile	Asp	Arg	Glu	Leu	His	Glu	
400						405				410						
AAT	GGG	GAA	CCT	CAT	CTC	CAT	GTG	CTT	GTT	CAG	TTC	GAA	GGA	AAG	TAC	247
Asn	Gly	Glu	Pro	His	Leu	His	Val	Leu	Val	Gln	Phe	Glu	Gly	Lys	Tyr	
415					420					425					430	
CAG	TGC	ACG	AAT	AAC	AGA	TTC	TTC	GAC	CTG	GTC	TCC	CCA	ACC	CGG	TCA	295
Gln	Cys	Thr	Asn	Asn	Arg	Phe	Phe	Asp	Leu	Val	Ser	Pro	Thr	Arg	Ser	
			435					440						445		
GCA	CAT	TTC	CAT	CCG	AAT	ATT	CAG	GGA	GCT	AAA	TCG	AGC	TCC	GAC	GTC	343
Ala	His	Phe	His	Pro	Asn	Ile	Gln	Gly	Ala	Lys	Ser	Ser	Ser	Asp	Val	
			450				455						460			
AAA	TCG	TAC	ATC	GAC	AAG	GAC	GGA	GAT	ACA	ATC	GAA	TGG	GGA	GAT	TTC	391
Lys	Ser	Tyr	Ile	Asp	Lys	Asp	Gly	Asp	Thr	Ile	Glu	Trp	Gly	Asp	Phe	
		465					470					475				
CAG	ATC	GAC	GGC	AGA	TCG	ATC	TGC	CAG	AGG	AGG	CCA	GCA	GTC	TGC	TAA	439
Gln	Ile	Asp	Gly	Arg	Ser	Ile	Cys	Gln	Arg	Arg	Pro	Ala	Val	Cys	*	
	480					485					490					
TGATTCATAT GCGAAAGCGT TAAATGCAAG TTCGGTTCAA TCTGCCTTAG CAGTTCTAAG																499
GGAAGAACAA CCAAAAGATT TTGTATTACA AAATCATAAC ATCCGCTCTA ACCTAGAACG																559
AATATTCGCA AAGGCTCCGG AACCGTGGGT TCCTCCATTT CAAGTCTCTT CTTTCACTAA																619
CGTTCCTGAC GAGATGCAGG AATGGGCGGA TAATTATTTT GGGACGGGTG CAGCTGCGCG																679
GCCAGAGAGA CCTGTAAGTA TCATCGTCGA GGGTGATTCA AGAACAGGGA AGACGATGTG																739
GGCACGTGCG TTAGGCCCCAC ATAACATCTT CAGTGGACAC CTAGACTTCA ATGGTCGAGT																799
CTTCTCGAAT GATGTGCAGT ATAACGTCAT TGATGACATC GCACCGCATT ATCTAAAGCT																859
AAAGCACTGG AAAGAATTGC TAGGGGCCCA GAAAGATTGG CAATCAAATT GCAAGTACGG																919
TAAGCCAGTT CAAATTAAAG GCGGAATCCC AGCAATCGTG CTTTGCAATC CTGGTGAGGG																979
TGCCAGCTAT AAAGAGTTCT TAGACAAAGC AGAAAATACA GGTCTAAAGA ACTGGACTGT																1039
CAAGAATGCG ATCTTCATCA CCCTCACAGC CCCCCTCTAT CAAGACAGCA CACAGGCAAG																1099
CCAAGAAACG GGCAATCAGA AGGCGCAGGG TGATCTACA GTGCGGGTGC TCCATCTACT																1159
TCCTAGG																1166

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met  Pro  Pro  Pro  Lys  Lys  Phe  Arg  Val  Gln  Ser  Lys  Asn  Tyr  Phe  Leu
 1          5          10          15

Thr  Tyr  Pro  Gln  Cys  Ser  Leu  Ser  Lys  Glu  Glu  Ala  Leu  Ser  Gln  Leu
          20          25          30

Gln  Asn  Leu  Asn  Thr  Pro  Val  Asn  Lys  Lys  Phe  Ile  Lys  Ile  Cys  Arg
          35          40          45

Glu  Leu  His  Glu  Asn  Gly  Glu  Pro  His  Leu  His  Val  Leu  Val  Gln  Phe
 50          55          60

Glu  Gly  Lys  Tyr  Gln  Cys  Thr  Asn  Asn  Arg  Phe  Phe  Asp  Leu  Val  Ser
 65          70          75          80

Pro  Thr  Arg  Ser  Ala  His  Phe  His  Pro  Asn  Ile  Gln  Gly  Ala  Lys  Ser
          85          90          95

Ser  Ser  Asp  Val  Lys  Ser  Tyr  Ile  Asp  Lys  Asp  Gly  Asp  Thr  Ile  Glu
          100          105          110

Trp  Gly  Asp  Phe  Gln  Ile  Asp  Gly  Arg  Ser  Ile  Cys  Gln  Arg  Arg  Pro
          115          120          125

Ala  Val  Cys  *
          130

```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Mottle Geminivirus
- (B) STRAIN: Florida

## (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Gilbertson, RL  
Hidayat, SH  
Paplomatas, EJ  
Rojas, MR  
Hou, YM  
Maxwell, DP
- (B) TITLE: Pseudorecombination between the infectious  
cloned DNA components of tomato mottle and bean  
dwarf mosaic geminiviruses.
- (C) JOURNAL: Journal of General Virology
- (D) VOLUME: 74
- (F) PAGES: 23-31

(3) DATE: 1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGATCTGCCA GAGGAGGCCA GCAGTCTGCT AATGATTCAT ATGCGAAAGC GTTAAATGCA	50
AGTTCGGTTC AATCTGCCTT AGCAGTTCTA AGGGAAGAAC AACCAAAGA TTTTGTATTA	120
CAAAATCATA ACATCCGCTC TAACCTAGAA CGAATATTCG CAAAGGCTCC GGAACCGTGG	180
GTTCTCCAT TTCAAGTCTC TTCTTTCCTT AACGTTCTCTG ACGAGATGCA GGAATGGGCG	240
GATAATTATT TCGGGACGGG TGCAGCTGCG CGGCCAGAGA GACCTGTAAG TATCATCGTC	300
GAGGGTGATT CAAGAACAGG GAAGACGATG TGGGCACGTG CGTTAGGCCC ACATAACTAT	360
CTCAGTGGAC ACCTAGACTT CAATGGTCGA GTCTTCTCGA ATGATGTGCA GTATAACGTC	420
ATTGATGACA TCGCACCGCA TTATCTAAAG CTAAAGCACT GGAAAGAATT GCTAGGGGCC	480
CAGAAAGATT GGCAATCAAA TTGCAAGTAC GGTAAGCCAG TTCAAATTAA AGGCGGAATC	540
CCAGCAATCG TGCTTTGCAA TCCTGGTGAG GGTGCCAGCT ATAAAGAGTT CTTAGACAAA	600
GCAGAAAATA CAGGTCTAAA GAACTGGACT GTCAAGAATG CGATCTTCAT CACCCTCACA	660
GGCCCCCTCT ATCAAGACAG CACACAGGCA AGCCAAGAAA CGGGCAATCA GAAGGCGCAG	720
GGTTGATCTA CAGTGCGGGT GCTCCATCTA CTTCCACTTA GACTGTGCGG GACATGGATT	780
CACGCACAGG GGAATCATC ACTGCACATC AGGCGGAGAA TGGCGTGTAT ATCTGGGAGC	840
TAAAAAATCC CCTTTATTTT AAGATACACA GGGTAGAGGA ACCACTGTAT ACCAGAACGA	900
GGGTATACCA CGTACAGATA CGGTTCAACC ACAACCTGAG GAAAGCGTTG CATCTCCACA	960
AAGCCTACCT GAACTTCCAA GTTTGGACGA CGTGGATGAC AGCTTCTGGA TCAATTTATT	1020
TAGCTAGATT TAGATATTTA GTCAACATGT ATCTAGATCA ATTAGGTGTT ATTTCAATAA	1080
ACAATGTAAT TAGAGCTGTA CGTTTCGCAA CAAACAGAGT GTATGTAAAT CATGTATTGG	1140
AGAATCATTC AATAAAATTC AAATTTTATT AATTCATGAT CGAATCATAA AAATAGATTC	1200
GAATTTTCAA AGTTGCATAT ACAGGGTTAG ACGCATGAGT GCATGC	1246

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

A. ORGANISM: FL-2549H

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TATCAAAGCT TGAGTAACTC ATCTGGAGTA CC

32

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Mottle Geminivirus
- (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGCATT TTT TGTAATAAGA AGGGGTACTC CAGATGAGTT ACTCCAATTG AGCCTTCTCA	60
AAC TTGCTCA TTCAATTGGA GTATTAGAGT AACTTATATA TAAGAACCCT CTATAGAACT	120
ATTAATCTGG TTCATACACG TGGCGGCCAT CCGATATAAT ATTACCGGAT GGCCGCGCGC	180
TTTTTTT TAA TCCGTACAGT CCAATACTCT CACATCCAAT CATAATGCGT CGTACAAGCC	240
TATATAT TTT CAACAAC TTG GGCCTTAAGT TGT TGGAGGC CCATTATAAA TTAAAGTGAT	300
CTTGGCCCAA TGTCTTTAAC TCAAAATGCC TAAGCGTGAT TTGCCATGGC GATCGATGGC	360
GGGAACCTCA AAGGTTAGCC GCAATGCTAA TTATTCTCCT CGTGCAGGTA TTAGGCCAAG	420
AATTAACAAG GCCGCTGAAT GGGTGAATCG GCCCATGTAT AGGAAGCCCA GGATCTATCG	480
GACTCTTAGT ACAACTGACG TGCCCGAGGG CTGTGAAGGC CCATGTAAGG TCCAGTCTTT	540
CGAACAGCGC CATGACATCT CACATATCGG TAAGGTCATG TGCATATCCG ATGTGACACG	600
TGGTAATGGC ATAACCCACC GTGTTGGTAA GCGTTTCTGT GTTAAGTCTG TGTATATCCT	660
TGGTAAGATT TGGATGGATG AGAACATCAA GCTCAAGAAC CACACGAATA GTGTCATGTT	720
CTGGTTGGTC AGAGATCGTA GACCCTATGG TACTCCAATG GATTTTGGAC AGGTGTTCAA	780
CATGTTGAT AACGAGCCTA GCACTGCTAC TGTCAAAAAC GATCTACGCG ATCGTTACCA	840
GGTCATGCAT AAGTTCTATG GCAAGGTGAC AGGTGGACAG TATGCCAGCA ACGAGCAGGC	900
TATAGTTAAG AGGTTCTGGA AGGTGAACAA TCATGTAGTC TATAATCATC AAGAGGCTGG	960

CAAGTACGAG AATCACACAG AGAAGCCCTT GTTATTGTAT ATGGCATGCA CTCATGCGTC	1020
TAACCCTGTA TATGCAACTT TGAAAATTCG AATCTATTTT TATGATTCTGA TCATGAATTA	1080
ATAAAATTTG AATTTTATTG AATGATTCTC CAATACATGA TTTACATACA CTCTGTTTGT	1140
TGCGAAACGT ACAGCTCTAA TTACATTGTT TATTGAAATA ACACCTAATT GATCTAGATA	1200
CATGTTGACT AAATATCTAA ATCTAGCTAA ATAAATTGAT CCAGAAGCTG TCATCCACGT	1260
CGTCCAAACT TGGAAGTTCA GGTAGGCTTT GTGGAGATGC AACGCTTTCC TCAGGTTGTG	1320
GTTGAACCGT ATCTGTACGT GGTATACCCT CGTTCTGGTA TACAGTGGTT CCTCTACCCT	1380
GTGTATCTTG AAATAAAGGG GATTTTTTAG CTCCCAGATA TACACGCCAT TCTCCGCCTG	1440
ATGTGCAGTG ATGAGTTCCC CTGTGCGTGA ATCCATGTCC CGCACAGTCT AAGTGGGAAGT	1500
AGATGGAGCA CCCGCACTGT AGATCAACCC TGCGCCTTCT GATTGCCCGT TTCTTGGCTT	1560
GCCTGTGTGC TGTCTTGATA GAGGGGGGCT GTGAGGGTGA TGAAGATCGC ATTCTTGACA	1620
GTCCAGTTCT TTAGACCTGT ATTTTCTGCT TTGTCTAAGA ACTCTTTATA GCTGGCACCC	1680
TCACCAGGAT TGCAAAGCAC GATTGCTGGG ATTCCGCCTT TAATTTGAAC TGGCTTACCG	1740
TACTTGCAAT TTGATTGCCA ATCTTTCTGG GCCCCTAGCA ATTCTTTCCA GTGCTTTAGC	1800
TTTAGATAAT GCGGTGCGAT GTCATCAATG ACGTTATACT GCACATCATT CGAGAAGACT	1860
CGACCATTGA AGTCTAGGTG TCCACTGAGA TAGTTATGTG GGCCTAACGC ACGTGCCAC	1920
ATCGTCTTCC CTGTTCTTGA ATCACCCTCG ACGATGATAC TTACAGGTCT CTCTGGCCGC	1980
GCAGCTGCAC CCGTCCCGAA ATAATTATCC GCCCATTCTT GCATCTCGTC AGGAACGTTA	2040
GTGAAAGAAG AGACTTGAAA TGGAGGAACC CACGGTCCG GAGCCTTTGC GAATATTCGT	2100
TCTAGGTTAG AGCGGATGTT ATGATTTTGT AATACAAAAT CTTTGGTTG TTCTTCCCTT	2160
AGAAGTCTA AGGCAGATTG AACCGAATT GCATTTAACG CTTTCGCATA TGAATCATTA	2220
GCAGACTGCT GGCCTCCTCT GGCAGATCTG CCGTCGATCT GGAAATCTCC CCATTGATT	2280
GTATCTCCGT CCTTGTCGAT GTACGATTTG ACGTCGGAGC TCGATTTAGC TCCCTGAATA	2340
TTCGGATGGA AATGTGCTGA CCGGGTTGGG GAGACCAGGT CGAAGAATCT GTTATTCGTG	2400
CACTGGTACT TTCCTTCGAA CTGAACAAGC ACATGGAGAT GAGGTTCCCC ATTTTCATGA	2460
AGCTCTCTGC AAATTTTGAT GAATTTCTTA TTGACTGGGG TATTTAGGTT TTGTAATTGG	2520
GAAAGTGCTT CTTCTTTAGA CAAAGAGCAC TGTGGATAAG TGAGGAAATA GTTCTTTGAC	2580
TGAACTCTAA ATTTCTTTGG TG	2602

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2540 base pairs



B TYPE: nucleic acid  
 C: STRANDEDNESS: single  
 D: TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Tomato Mottle Geminivirus  
 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTGGCATT TT TGTAATAAGA AGGGGTACTC CAGATGAGTT ACTCCAATTG AGCCTTCTCA	60
AACTTGCTCA TTCAATTGGA GTATTAGAGT AACTTATATA TAAGAACCCT CTATAGAATT	120
ATTAATCTGG TTCATACACG TGGCGGCCAT CCGATATAAT ATTACCGGAT GGCCGCGCCC	180
CCCCCCTTT TATACGCGCG CCTCTTTTGT CGTATTTCCA CGCTTCTTCC TGTTGGTGCG	240
TATCCTTCAC TTCCCATCTT TTTGAGTAGC CTTTAATTTG AATTAAAGGT TAAAACTTTA	300
TCGCGATGAC TAATCATATC ACATTGACCA TGTGAAGGAC GTGGCATTAT TTCGACCATG	360
CTGCTGAGTT TATTTGCTAT TATTGTTCTA TCCATAATCT ATATATTGGA TTGGTCAGGA	420
ATATTTTGTT TATCCAACTC AGCTGCATAC CACGTTTATA TCGTTAGCTA AATTTTGATT	480
AATCTTAGTT AAGTGTTTGA CTATGTATCC TTTAAAGTGT AAACGTGGTT TATCATATTC	540
AAATCGAAGA TTAACTCAC GTAATAATGT GTTTAACCGT CCAGTTTCTG GTAAGAGACA	600
TGATGGAAAG CGTCGGGGAG GTAATTTCTG GAAGCCCAAT GATGAGCCCA AGATGTTAGC	660
CCAACGCATA CATGAGAATC AGTATGGGCC TGAATTTGTA TTGGCCCATATA ACTCAGCTAT	720
CTCCACATTT ATCAGTTATC CCATCTTGGG CAAGTCCGAA GCCAGTCGAA GTAGGTCCTA	780
TATCAAGTTG AAACGTCTTC GTTTCAAAGG GACTGTGAAG ATTGAGCGTG TTCAATCTGA	840
TTTGAACATG GATGGCTTTA TGCCTAAAGT CGAAGGAGTA TTCTCTATGG TTGTTGTTGT	900
GGATCGTAAA CCACACTTGG GTCCCTCCGG GTGTTTGCAAT ACATTCGACG AGCTATTTGG	960
TGCAAGGATC AATAGTCATG GCAACCTCAC TATAGTACCT TCTCTGAAAG ACCGCTTCTA	1020
CATTAGACAT GTGTTCAAGC GAGTGCTCTC AGTTGAGAAG GATACGTTGA TGGTGACGT	1080
TGAAGGATCC ACAACACTCT CTAACAGGCG TTACAACTGC TGGTCTACGT TTAAAGACCT	1140
TGATCGTGAA TCATGCAAGG GTGTTTATGA TAACATTAGC AAGAACGCCT TGTTAGTTTA	1200
TTATTGCTGG ATGTCTGACA CGCCTCGAA TGCATCCTCT TTTGTATCTT TTGATCTTGA	1260
TTATATTGGT TAACTTAACG AAGTGTGTTT GTCTAAAGAT GATTAAAAAA ATGAAAATGT	1320

AAAAATAAAA TTTTATTTTA ATG6TTTCGT GTGASAC6CC TTACAATTAC TATTAATACA	1320
TTTCATGGACC GTAGTCCGTA TTAATTCATT CAACTGTCCC ATAGACATTG TAATGTTGGA	1440
CTCTGTTCTC TGGGCCCCCA CAATAGAAGC AGACTCTCCC GGGTCCAGTA TGCCTGTTCC	1500
TAGCCTGTTT AGATGTCTGT ACGGGTGGAG TTCGTTCTCC ACATCTGAGT CCGCATCTGA	1560
ATGCCCTATG CCTATTGTAC TCCTTGAAGC CCATGACTCA CCAGGCCTGA TCTCAATTGG	1620
ACCTCTAAGC CCAAGTCTGG ACATGGACGC GCATCTAATG GGCTTCCTCT CCCATTTACC	1680
GTAATCCACA TGGGAAAAGT CCACATCTTT ATCTGTGAAC TGTTTGGAACA GGATTTTTAC	1740
TGTTGGTGCC CGGAAGGGGA TGTCTACTGA GTGTTTTGCT GTGGACAATT TCAGCTTCCC	1800
CTTAAACTTG GCGAAGTGGG TCCGTTGATG AACATTCGTA TCGCAAACCC TGTAATACAA	1860
TTTCCATGGA ATTGGGTCTT TCAAGGAGAA GAAGGAAGCT GAGAAATAGT GGAGATCTAT	1920
GTTGCACCTG ATCGGAAATG TCCATGATGC CTGTAAAGAC TCATTCTCCG TCATTCTTTT	1980
GTCGTGAATC TCCACTATTA CCGACCCAGT GGCCTTTATT GGTACTTGTT GTCTGTACTC	2040
TATGACACAG TGGTCGATTT TCATGCAGCT ACGGCTGAGC CTAGCGGTTA ACTGCGACGC	2100
CGTGGACGGA AATTGCAGTA TTATTTCACT TAGGTCATGA GAAAGCTGAT ATTCGTCACG	2160
GTGTGCATCT ATGTAGTTGA ATGCGCTAGG AGGATTAAT AACTGAGAAT CCATATGAAG	2220
AAAATAAGGC CGCGCAGGAC TGATTGCTGA AGTTGAATCA GAAAGAAGTC GAACAAGCTA	2280
TGAAACGGCA GTTTCGAACT CGAAGAAGAA AGACAGCCAA CTATATTTTC TTTTTTCCAA	2340
GAATTCAGCT GTGCTGAATA TAAAGTTTAT GAAGAGCGGA AATGAAAAAA AGTATATCAG	2400
GATTTCGAAGT GTTTGAGAAA GAAAAGAAAT ATGAAAGAGA ATTTTGAGTA AATTTGAGTA	2460
AGAAGGAATT TGTATATGAA CTAAGAAACC TAGGGTTGAT GGGTATTTAA ATTGGTAAAG	2520
TGTTTCATCCC ATGAGATAGA	2540

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) FRAGMENT TYPE: N-terminal

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Yellow Leaf Curl Virus

3 STRAIN: Israel

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 37..1110

## (x) PUBLICATION INFORMATION:

(A) AUTHORS: Navot, N  
 Pichersky, R  
 Zeidan, D  
 Zamir, D  
 Czosnek, H  
 (B) TITLE: Tomato yellow leaf curl virus: A  
 whitefly-transmitted geminivirus with a single  
 genomic component.  
 (C) JOURNAL: Virology  
 (D) VOLUME: 185  
 (F) PAGES: 151-168  
 (G) DATE: 1991

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA	54
Met Pro Arg Leu Phe Lys	
135	
ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT	102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser	
140 145 150	
AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT	150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn	
155 160 165 170	
AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA	198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro	
175 180 185	
CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC	246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn	
190 195 200	
CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT	294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His	
205 210 215	
CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG	342
Pro Asn Ile Gln Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val	
220 225 230	
GAG AAA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC	390
Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly	
235 240 245 250	
AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA	438
Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu	
255 260 265	
GCA CTC AAT TCA GGC AGT ATA TCC GAG GCC CTC AAT ATA TTA AAA GAG	486
Ala Leu Asn Ser Gly Ser Ile Ser Glu Ala Leu Asn Ile Leu Lys Glu	

270	275	280	
AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn 285 290 295			534
TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe 300 305 310			582
CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val 315 320 325 330			630
GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser 335 340 345			678
ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC AAA ACA ATG TGG GCC AGG Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Lys Thr Met Trp Ala Arg 350 355 360			726
TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro 365 370 375			774
AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT GAT GAC GTA AAC Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Asp Asp Val Asn 380 385 390			822
CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATT TGG GCC CAG AGG GAC Pro His Tyr Leu Lys His Phe Lys Glu Phe Ile Trp Ala Gln Arg Asp 395 400 405 410			870
TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly 415 420 425			918
ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg 430 435 440			966
GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu 445 450 455			1014
AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile 460 465 470			1062
AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala * 475 480 485 490			1110
GCGTGTAGAC CTAGACTGTG GCTGCTCATA CTACC			1145

(2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:

A) LENGTH 158 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
 1           5           10           15
Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
          20           25           30
Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
          35           40           45
His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
          50           55           60
Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
          65           70           75           80
Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
          85           90           95
Asp Val Lys Thr Tyr Val Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly
          100          105          110
Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
          115          120          125
Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Ile Ser Glu Ala
          130          135          140
Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
          145          150          155          160
His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
          165          170          175
Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
          180          185          190
Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
          195          200          205
Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
          210          215          220
Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
          225          230          235          240
His Leu Asp Leu Ser Pro Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn
          245          250          255
Val Ile Asp Asp Val Asn Pro His Tyr Leu Lys His Phe Lys Glu Phe
          260          265          270
Ile Trp Ala Gln Arg Asp Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro

```

275                      280                      285  
 Ile Gln Ile Lys Gly Gly Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly  
 290                      295                      300  
 Pro Thr Ser Ser Tyr Arg Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser  
 305                      310                      315                      320  
 Leu Lys Asn Trp Ala Leu Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu  
 325                      330                      335  
 Pro Leu Phe Ala Ser Ile Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu  
 340                      345                      350  
 Glu Thr Asn Lys Ala \*  
 355

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PTYIRC4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTC

33

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PTYCIV

1679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

SGTAGTATGA GGATCCACAG TCTAGGTCTA CACGCTTAC

39

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato Yellow Leaf Curl Geminivirus
- (B) STRAIN: Israel

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 37..1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC	ATG CCT CGT TTA TTT AAA	54
	Met Pro Arg Leu Phe Lys	
	360	
ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT		102
Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser		
365 370 375 380		
AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT		150
Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn		
385 390 395		
AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA		198
Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro		
400 405 410		
CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC		246
His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn		
415 420 425		
CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT		294
Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His		
430 435 440		
CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG		342
Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val		
445 450 455 460		
GAG CGA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC		390
Glu Arg Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly		

85



705

710

715

GCCTGTAGAC CTAGACTGTG GCTGCTCATA CTACC

1145

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Pro Arg Leu Phe Lys Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr
 1           5           10           15
Pro Asn Cys Ser Leu Ser Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys
          20           25           30
Leu Glu Thr Pro Thr Asn Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu
          35           40           45
His Glu Asn Gly Glu Pro His Leu His Val Leu Ile Gln Phe Glu Gly
          50           55           60
Lys Tyr Gln Cys Lys Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Asn
          65           70           75           80
Arg Ser Ala His Phe His Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr
          85           90           95
Asp Val Lys Thr Tyr Val Glu Arg Asp Gly Asn Phe Ile Asp Phe Gly
          100          105          110
Val Ser Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala
          115          120          125
Asn Asp Ala Tyr Ala Glu Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala
          130          135          140
Leu Asn Ile Leu Lys Glu Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe
          145          150          155          160
His Asn Leu Ser Ser Asn Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu
          165          170          175
Val Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asn Gln Val Pro Asp
          180          185          190
Glu Leu Glu Glu Trp Val Ala Glu Asn Val Val Tyr Ser Ala Ala Arg
          195          200          205
Pro Trp Arg Pro Ile Ser Ile Val Ile Glu Gly Asp Ser Arg Thr Gly
          210          215          220
Lys Thr Met Trp Ala Arg Ser Leu Gly Pro His Asn Tyr Leu Cys Gly
          225          230          235          240

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:25:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: C1V2467
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTTTCCGTCT CGCTCCACGT AGG

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (v) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Tomato Yellow Leaf Curl Virus  
 (B) STRAIN: Israel
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 37..1110
- (x) PUBLICATION INFORMATION:  
 (A) AUTHORS: Navot, N  
 Pichersky, R  
 Zeidan, D  
 Zamir, D  
 Czosnek, H  
 (B) TITLE: Tomato yellow leaf curl virus: A  
 whitefly-transmitted geminivirus with a single  
 genomic component.  
 (C) JOURNAL: Virology  
 (D) VOLUME: 185  
 (F) PAGES: 151-168  
 (G) DATE: 1991
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA | 54  |
| Met Pro Arg Leu Phe Lys                                         |     |
| 360                                                             |     |
| ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT | 102 |
| Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser |     |
| 365 370 375 380                                                 |     |
| AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT | 150 |
| Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn |     |
| 385 390 395                                                     |     |
| AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA | 198 |
| Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro |     |
| 400 405 410                                                     |     |
| CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC | 246 |
| His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn |     |
| 415 420 425                                                     |     |
| CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT | 294 |
| Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His |     |
| 430 435 440                                                     |     |
| CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG | 342 |
| Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val |     |
| 445 450 455 460                                                 |     |
| GAG AAA GAC GGA AAC TTC ATT GAT TTT GGA GTT TCC CAA ATC GAT GGC | 390 |
| Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly |     |
| 465 470 475                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AGA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GCC GAA<br>Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu<br>480 485 490     | 433  |
| GCA CTC AAT TCA GGC AGT AAA TCC GAG GCC CTC AAT ATA TTA AAA GAG<br>Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala Leu Asn Ile Leu Lys Glu<br>495 500 505     | 486  |
| AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT<br>Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn<br>510 515 520     | 534  |
| TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT<br>Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe<br>525 530 535 540 | 582  |
| CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC<br>Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val<br>545 550 555     | 630  |
| GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT<br>Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser<br>560 565 570     | 678  |
| ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC GCA ACA ATG TGG GCC AGG<br>Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Ala Thr Met Trp Ala Arg<br>575 580 585     | 726  |
| TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA<br>Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro<br>590 595 600     | 774  |
| AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT GAT GAC GTA GAC<br>Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Asp Asp Val Asp<br>605 610 615 620 | 822  |
| CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATG GGG GCC CAG AGG GAC<br>Pro His Tyr Leu Lys His Phe Lys Glu Phe Met Gly Ala Gln Arg Asp<br>625 630 635     | 870  |
| TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA<br>Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly<br>640 645 650     | 918  |
| ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG<br>Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg<br>655 660 665     | 966  |
| GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC<br>Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu<br>670 675 680     | 1014 |
| AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC<br>Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile<br>685 690 695 700 | 1062 |
| AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA<br>Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala *<br>705 710 715       | 1110 |

GGGTGTAGAC CTAGACTGTG GGTGCTCATA CTACC

1145

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met  Pro  Arg  Leu  Phe  Lys  Ile  Tyr  Ala  Lys  Asn  Tyr  Phe  Leu  Thr  Tyr
 1          5          10          15
Pro  Asn  Cys  Ser  Leu  Ser  Lys  Glu  Glu  Ala  Leu  Ser  Gln  Leu  Lys  Lys
          20          25          30
Leu  Glu  Thr  Pro  Thr  Asn  Lys  Lys  Tyr  Ile  Lys  Val  Cys  Lys  Glu  Leu
          35          40          45
His  Glu  Asn  Gly  Glu  Pro  His  Leu  His  Val  Leu  Ile  Gln  Phe  Glu  Gly
          50          55          60
Lys  Tyr  Gln  Cys  Lys  Asn  Gln  Arg  Phe  Phe  Asp  Leu  Val  Ser  Pro  Asn
          65          70          75          80
Arg  Ser  Ala  His  Phe  His  Pro  Asn  Ile  Gln  Ala  Ala  Lys  Ser  Ser  Thr
          85          90          95
Asp  Val  Lys  Thr  Tyr  Val  Glu  Lys  Asp  Gly  Asn  Phe  Ile  Asp  Phe  Gly
          100          105          110
Val  Ser  Gln  Ile  Asp  Gly  Arg  Ser  Ala  Arg  Gly  Gly  Gln  Gln  Ser  Ala
          115          120          125
Asn  Asp  Ala  Tyr  Ala  Glu  Ala  Leu  Asn  Ser  Gly  Ser  Lys  Ser  Glu  Ala
          130          135          140
Leu  Asn  Ile  Leu  Lys  Glu  Lys  Ala  Pro  Lys  Asp  Tyr  Ile  Leu  Gln  Phe
          145          150          155          160
His  Asn  Leu  Ser  Ser  Asn  Leu  Asp  Arg  Ile  Phe  Ser  Pro  Pro  Leu  Glu
          165          170          175
Val  Tyr  Val  Ser  Pro  Phe  Leu  Ser  Ser  Ser  Phe  Asn  Gln  Val  Pro  Asp
          180          185          190
Glu  Leu  Glu  Glu  Trp  Val  Ala  Glu  Asn  Val  Val  Tyr  Ser  Ala  Ala  Arg
          195          200          205
Pro  Trp  Arg  Pro  Ile  Ser  Ile  Val  Ile  Glu  Gly  Asp  Ser  Arg  Thr  Gly
          210          215          220
Ala  Thr  Met  Trp  Ala  Arg  Ser  Leu  Gly  Pro  His  Asn  Tyr  Leu  Cys  Gly
          225          230          235          240

```



iv ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Tomato Yellow Leaf Curl Virus

(B) STRAIN: Israel

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 37..1110

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Navot, N  
Pichersky, R  
Zeidan, D  
Zamir, D  
Czosnek, H

(B) TITLE: Tomato yellow leaf curl virus: A  
whitefly-transmitted geminivirus with a single  
genomic component.

(C) JOURNAL: Virology

(D) VOLUME: 185

(F) PAGES: 151-168

(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCCATAGAGC TTTGAGGGAT CCCGATTCAT TTCAAC ATG CCT CGT TTA TTT AAA | 54  |
| Met Pro Arg Leu Phe Lys                                         |     |
| 360                                                             |     |
| ATA TAT GCC AAA AAT TAT TTC CTA ACA TAT CCC AAT TGT TCT CTC TCT | 102 |
| Ile Tyr Ala Lys Asn Tyr Phe Leu Thr Tyr Pro Asn Cys Ser Leu Ser |     |
| 365 370 375 380                                                 |     |
| AAA GAG GAA GCA CTT TCC CAA TTA AAA AAA CTA GAA ACC CCA ACA AAT | 150 |
| Lys Glu Glu Ala Leu Ser Gln Leu Lys Lys Leu Glu Thr Pro Thr Asn |     |
| 385 390 395                                                     |     |
| AAA AAA TAC ATC AAA GTT TGC AAA GAA CTC CAC GAG AAT GGG GAA CCA | 198 |
| Lys Lys Tyr Ile Lys Val Cys Lys Glu Leu His Glu Asn Gly Glu Pro |     |
| 400 405 410                                                     |     |
| CAT CTC CAT GTG CTT ATC CAA TTC GAA GGC AAA TAC CAA TGT AAG AAC | 246 |
| His Leu His Val Leu Ile Gln Phe Glu Gly Lys Tyr Gln Cys Lys Asn |     |
| 415 420 425                                                     |     |
| CAA CGG TTC TTC GAC TTG GTA TCC CCA AAC AGG TCA GCA CAT TTC CAT | 294 |
| Gln Arg Phe Phe Asp Leu Val Ser Pro Asn Arg Ser Ala His Phe His |     |
| 430 435 440                                                     |     |
| CCG AAC ATT CAG GCA GCT AAG AGC TCA ACA GAT GTC AAG ACC TAC GTG | 342 |
| Pro Asn Ile Gln Ala Ala Lys Ser Ser Thr Asp Val Lys Thr Tyr Val |     |
| 445 450 455 460                                                 |     |
| GAG AAA GAC GGA AAC TTC ATT CAT TTT GGA GTT TCC CAA ATC GAT GGC | 390 |
| Glu Lys Asp Gly Asn Phe Ile Asp Phe Gly Val Ser Gln Ile Asp Gly |     |
| 465 470 475                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ACA TCA GCT AGA GGA GGT CAG CAA TCT GCC AAC GAC GCA TAT GGC GAA<br>Arg Ser Ala Arg Gly Gly Gln Gln Ser Ala Asn Asp Ala Tyr Ala Glu<br>480 485 490     | 433  |
| GCA CTC AAT TCA GGC AGT AAA TCC GAG GCC CTC AAT ATA TTA AAA GAG<br>Ala Leu Asn Ser Gly Ser Lys Ser Glu Ala Leu Asn Ile Leu Lys Glu<br>495 500 505     | 486  |
| AAG GCC CCA AAG GAC TAT ATT TTA CAA TTT CAT AAT TTA AGT TCA AAT<br>Lys Ala Pro Lys Asp Tyr Ile Leu Gln Phe His Asn Leu Ser Ser Asn<br>510 515 520     | 534  |
| TTA GAT AGG ATT TTT AGT CCT CCT TTA GAA GTT TAT GTT TCT CCA TTT<br>Leu Asp Arg Ile Phe Ser Pro Pro Leu Glu Val Tyr Val Ser Pro Phe<br>525 530 535 540 | 582  |
| CTT TCT TCT TCT TTT AAT CAA GTT CCA GAT GAA CTT GAA GAG TGG GTC<br>Leu Ser Ser Ser Phe Asn Gln Val Pro Asp Glu Leu Glu Glu Trp Val<br>545 550 555     | 630  |
| GCC GAG AAC GTC GTG TAT TCC GCT GCG CGG CCA TGG AGA CCC ATA AGT<br>Ala Glu Asn Val Val Tyr Ser Ala Ala Arg Pro Trp Arg Pro Ile Ser<br>560 565 570     | 678  |
| ATT GTC ATT GAG GGT GAT AGC AGA ACA GGC AAA ACA ATG TGG GCC AGG<br>Ile Val Ile Glu Gly Asp Ser Arg Thr Gly Lys Thr Met Trp Ala Arg<br>575 580 585     | 726  |
| TCT CTA GGC CCA CAT AAT TAT TTA TGT GGA CAT CTA GAC CTA AGC CCA<br>Ser Leu Gly Pro His Asn Tyr Leu Cys Gly His Leu Asp Leu Ser Pro<br>590 595 600     | 774  |
| AAG GTG TAC AGT AAT GAT GCG TGG TAC AAC GTC ATT AGA GAC GTA GAC<br>Lys Val Tyr Ser Asn Asp Ala Trp Tyr Asn Val Ile Arg Asp Val Asp<br>605 610 615 620 | 822  |
| CCG CAT TAT TTA AAG CAC TTC AAG GAA TTC ATG GGG GCC CAG AGG GAC<br>Pro His Tyr Leu Lys His Phe Lys Glu Phe Met Gly Ala Gln Arg Asp<br>625 630 635     | 870  |
| TGG CAA AGC AAC ACA AAG TAC GGG AAG CCC ATT CAA ATT AAA GGG GGA<br>Trp Gln Ser Asn Thr Lys Tyr Gly Lys Pro Ile Gln Ile Lys Gly Gly<br>640 645 650     | 918  |
| ATT CCC ACT ATC TTC CTC TGC AAT CCA GGA CCT ACC TCC TCA TAT AGG<br>Ile Pro Thr Ile Phe Leu Cys Asn Pro Gly Pro Thr Ser Ser Tyr Arg<br>655 660 665     | 966  |
| GAA TAT CTA GAC GAA GAA AAA AAC ATA TCC TTG AAA AAT TGG GCT CTC<br>Glu Tyr Leu Asp Glu Glu Lys Asn Ile Ser Leu Lys Asn Trp Ala Leu<br>670 675 680     | 1014 |
| AAG AAT GCA ACC TTC GTC ACC CTC TAC GAG CCA CTG TTC GCA AGT ATC<br>Lys Asn Ala Thr Phe Val Thr Leu Tyr Glu Pro Leu Phe Ala Ser Ile<br>685 690 695 700 | 1062 |
| AAT CAA GGT CCA ACA CAA GAT AGC CAA GAA GAA ACC AAT AAG GCG TAA<br>Asn Gln Gly Pro Thr Gln Asp Ser Gln Glu Glu Thr Asn Lys Ala *<br>705 710 715       | 1110 |



GCCTGTAGAC CTAGACTGTG GCTGCTCATA CTACC

1143

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Arg | Leu | Phe | Lys | Ile | Tyr | Ala | Lys | Asn | Tyr | Phe | Leu | Thr | Tyr | 1   | 5   | 10  | 15  |
| Pro | Asn | Cys | Ser | Leu | Ser | Lys | Glu | Glu | Ala | Leu | Ser | Gln | Leu | Lys | Lys | 20  | 25  | 30  |     |
| Leu | Glu | Thr | Pro | Thr | Asn | Lys | Lys | Tyr | Ile | Lys | Val | Cys | Lys | Glu | Leu | 35  | 40  | 45  |     |
| His | Glu | Asn | Gly | Glu | Pro | His | Leu | His | Val | Leu | Ile | Gln | Phe | Glu | Gly | 50  | 55  | 60  |     |
| Lys | Tyr | Gln | Cys | Lys | Asn | Gln | Arg | Phe | Phe | Asp | Leu | Val | Ser | Pro | Asn | 65  | 70  | 75  | 80  |
| Arg | Ser | Ala | His | Phe | His | Pro | Asn | Ile | Gln | Ala | Ala | Lys | Ser | Ser | Thr | 85  | 90  | 95  |     |
| Asp | Val | Lys | Thr | Tyr | Val | Glu | Lys | Asp | Gly | Asn | Phe | Ile | Asp | Phe | Gly | 100 | 105 | 110 |     |
| Val | Ser | Gln | Ile | Asp | Gly | Arg | Ser | Ala | Arg | Gly | Gly | Gln | Gln | Ser | Ala | 115 | 120 | 125 |     |
| Asn | Asp | Ala | Tyr | Ala | Glu | Ala | Leu | Asn | Ser | Gly | Ser | Lys | Ser | Glu | Ala | 130 | 135 | 140 |     |
| Leu | Asn | Ile | Leu | Lys | Glu | Lys | Ala | Pro | Lys | Asp | Tyr | Ile | Leu | Gln | Phe | 145 | 150 | 155 | 160 |
| His | Asn | Leu | Ser | Ser | Asn | Leu | Asp | Arg | Ile | Phe | Ser | Pro | Pro | Leu | Glu | 165 | 170 | 175 |     |
| Val | Tyr | Val | Ser | Pro | Phe | Leu | Ser | Ser | Ser | Phe | Asn | Gln | Val | Pro | Asp | 180 | 185 | 190 |     |
| Glu | Leu | Glu | Glu | Trp | Val | Ala | Glu | Asn | Val | Val | Tyr | Ser | Ala | Ala | Arg | 195 | 200 | 205 |     |
| Pro | Trp | Arg | Pro | Ile | Ser | Ile | Val | Ile | Glu | Gly | Asp | Ser | Arg | Thr | Gly | 210 | 215 | 220 |     |
| Lys | Thr | Met | Trp | Ala | Arg | Ser | Leu | Gly | Pro | His | Asn | Tyr | Leu | Cys | Gly | 225 | 230 | 235 | 240 |
| His | Leu | Asp | Leu | Ser | Pro | Lys | Val | Tyr | Ser | Asn | Asp | Ala | Trp | Tyr | Asn |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:31:

(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iv) ANTI-SENSE: NO

(A) ORGANISM: C1V2000

GGGTCTACGT CTCTAATGAC GTTGTACC

28

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE

(A) ORGANISM: PTYC2V1439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTGTGGAT CCCATTACCT TCCTGATGTT GTGG

34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PTYARIV466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTAGGATCCT ATATCTGTTG TAAGGGC

27

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PTYARIC1046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTAACTAATG CAGGATCCTA CATTCCAGAG GGC

33

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PTYC2c1814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAACGGATCC TTGAAAAATT GGGC

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PYTV1v1164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTACGAGAAC CATACTGAAA ACGCCT

26

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PTYC1c2196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAATCTGCAG ATGAACTAGA AGAGTGGG

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "Oligonucleotide Primer  
PTYC3c1320"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
GGTTCTGCAG CAGAGCAGTT GATCATGTAT TG 32

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "Oligonucleotide Primer  
PTYC1v2182"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
TAGGCCATGG CCGCGCAGCG GAATACACG 29

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "Oligonucleotide Primer  
PTYC1V2406"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGTTCGCGAG ATTGGGCATA TGCGTCGT

23

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Oligonucleotide Primer  
PTYC1c2140"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATTTCATGG AGACCCATAA GTATTGTC

28

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "Oligonucleotide Primer  
PTYCv1707"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTAGTATGA GGATCCACAG TCTAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1183 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bean Golden Mosaic Geminivirus

B STRAIN: Type II Isolates  
C: INDIVIDUAL ISOLATE: Guatemala

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1062

## (x) PUBLICATION INFORMATION:

(A) AUTHORS: Faria, JC  
Gilbertson, RL  
Hanson, SF  
Morales, FJ  
Ahlquist, P  
Loniello, AO  
Maxwell, D  
(B) TITLE: Bean Golden Mosaic Geminivirus Type II  
Isolates from the Dominican Republic and  
Guatemala: Nucleotide Sequences, Infectious  
Pseudorecombinants, and Phylogenetic Relationships  
(C) JOURNAL: Phytopathology  
(D) VOLUME: 84  
(E) ISSUE: 3  
(F) PAGES: 321-329  
(G) DATE: 1994

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC | 48  |
| Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu |     |
| 360 365 370                                                     |     |
| ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT | 96  |
| Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu |     |
| 375 380 385 390                                                 |     |
| CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG | 144 |
| Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu |     |
| 395 400 405                                                     |     |
| GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC | 192 |
| Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe |     |
| 410 415 420                                                     |     |
| GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC | 240 |
| Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser |     |
| 425 430 435                                                     |     |
| TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA | 288 |
| Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser |     |
| 440 445 450                                                     |     |
| AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA | 336 |
| Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu |     |
| 455 460 465 470                                                 |     |
| TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG | 384 |
| Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln |     |
| 475 480 485                                                     |     |
| TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA | 432 |

|            |            |            |            |            |            |            |     |     |     |     |     |     |     |     |     |  |      |
|------------|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Ser        | Ala        | Asn        | Asp        | Ser        | Tyr        | Ala        | Lys | Ala | Leu | Asn | Ala | Asp | Ser | Ile | Glu |  |      |
|            |            | 490        |            |            |            |            | 495 |     |     |     |     | 500 |     |     |     |  |      |
| TCT        | GCC        | TTG        | ACA        | ATA        | TTG        | AAG        | GAA | GAA | CAA | CCG | AAA | GAT | TAC | GTC | CTT |  | 480  |
| Ser        | Ala        | Leu        | Thr        | Ile        | Leu        | Lys        | Glu | Glu | Gln | Pro | Lys | Asp | Tyr | Val | Leu |  |      |
|            |            | 505        |            |            |            |            | 510 |     |     |     |     | 515 |     |     |     |  |      |
| CAA        | CAT        | CAC        | AAC        | ATC        | CGT        | TCT        | AAT | CTC | GAA | CGG | ATC | TTC | GTC | AAA | GTG |  | 529  |
| Gln        | His        | His        | Asn        | Ile        | Arg        | Ser        | Asn | Leu | Glu | Arg | Ile | Phe | Val | Lys | Val |  |      |
|            |            | 520        |            |            |            | 525        |     |     |     |     | 530 |     |     |     |     |  |      |
| CCG        | GAA        | CCA        | TGG        | GTT        | CCT        | CCA        | TTT | CCG | TTG | TCA | TCA | TTC | ATC | AAT | GTT |  | 576  |
| Pro        | Glu        | Pro        | Trp        | Val        | Pro        | Pro        | Phe | Pro | Leu | Ser | Ser | Phe | Ile | Asn | Val |  |      |
| 535        |            |            |            |            | 540        |            |     |     |     | 545 |     |     |     |     | 550 |  |      |
| CCG        | GTT        | GTT        | ATG        | CAA        | GAA        | TGG        | GTT | GAC | GAC | TAT | TTC | GGA | AGG | GGT | TCC |  | 624  |
| Pro        | Val        | Val        | Met        | Gln        | Glu        | Trp        | Val | Asp | Asp | Tyr | Phe | Gly | Arg | Gly | Ser |  |      |
|            |            |            |            | 555        |            |            |     | 560 |     |     |     |     |     | 565 |     |  |      |
| GCT        | GCG        | CGG        | CCG        | GAA        | AGA        | CCT        | ATT | AGT | ATC | ATC | GTC | GAA | GGT | GAT | TCA |  | 672  |
| Ala        | Ala        | Arg        | Pro        | Glu        | Arg        | Pro        | Ile | Ser | Ile | Ile | Val | Glu | Gly | Asp | Ser |  |      |
|            |            |            | 570        |            |            |            |     | 575 |     |     |     |     |     | 580 |     |  |      |
| CGA        | ACC        | GGA        | AAG        | ACA        | ATG        | TGG        | GCT | CGT | GCA | TTA | GGA | CCA | CAT | AAT | TAT |  | 720  |
| Arg        | Thr        | Gly        | Lys        | Thr        | Met        | Trp        | Ala | Arg | Ala | Leu | Gly | Pro | His | Asn | Tyr |  |      |
|            |            | 585        |            |            |            |            | 590 |     |     |     |     | 595 |     |     |     |  |      |
| TTG        | AGC        | GGT        | CAT        | TTG        | GAC        | TTT        | AAT | TCA | CGT | GTC | TAT | TCC | AAC | GCA | GTG |  | 768  |
| Leu        | Ser        | Gly        | His        | Leu        | Asp        | Phe        | Asn | Ser | Arg | Val | Tyr | Ser | Asn | Ala | Val |  |      |
|            | 600        |            |            |            |            | 605        |     |     |     |     | 610 |     |     |     |     |  |      |
| GAA        | TAC        | AAC        | GTC        | ATT        | GAT        | GAC        | ATA | AGC | CCC | AAT | TAT | TTG | AAG | TTA | AAG |  | 816  |
| Glu        | Tyr        | Asn        | Val        | Ile        | Asp        | Asp        | Ile | Ser | Pro | Asn | Tyr | Leu | Lys | Leu | Lys |  |      |
| 615        |            |            |            |            | 620        |            |     |     |     | 625 |     |     |     |     | 630 |  |      |
| CAC        | TGG        | AAA        | GAA        | CTA        | ATT        | GGG        | GCA | CAA | AAG | GAC | TGG | CAA | TCT | AAC | TGT |  | 864  |
| His        | Trp        | Lys        | Glu        | Leu        | Ile        | Gly        | Ala | Gln | Lys | Asp | Trp | Gln | Ser | Asn | Cys |  |      |
|            |            |            |            | 635        |            |            |     |     | 640 |     |     |     |     | 645 |     |  |      |
| AAA        | TAT        | GGA        | AAG        | CCG        | GTT        | CAA        | ATT | AAA | GGA | GGA | ATA | CCA | TCA | ATC | GTG |  | 912  |
| Lys        | Tyr        | Gly        | Lys        | Pro        | Val        | Gln        | Ile | Lys | Gly | Gly | Ile | Pro | Ser | Ile | Val |  |      |
|            |            |            | 650        |            |            |            |     | 655 |     |     |     |     |     | 660 |     |  |      |
| TTG        | TGC        | AAT        | CCA        | GGT        | GAG        | GGT        | TCC | AGT | TAT | AAA | GAC | TTC | CTC | GAC | AAA |  | 960  |
| Leu        | Cys        | Asn        | Pro        | Gly        | Glu        | Gly        | Ser | Ser | Tyr | Lys | Asp | Phe | Leu | Asp | Lys |  |      |
|            |            | 665        |            |            |            |            | 670 |     |     |     |     | 675 |     |     |     |  |      |
| GAA        | GAA        | AAC        | CGA        | GCT        | TTA        | CAC        | AAC | TGG | ACT | ATT | CAT | AAT | GCG | ATC | TTC |  | 1008 |
| Glu        | Glu        | Asn        | Arg        | Ala        | Leu        | His        | Asn | Trp | Thr | Ile | His | Asn | Ala | Ile | Phe |  |      |
|            | 680        |            |            |            |            | 685        |     |     |     |     | 690 |     |     |     |     |  |      |
| GTC        | ACC        | CTC        | ACA        | GCC        | CCC        | CTC        | TAT | CAA | AGC | ACA | ACA | CAG | GAT | TGC | CAA |  | 1056 |
| Val        | Thr        | Leu        | Thr        | Ala        | Pro        | Leu        | Tyr | Gln | Ser | Thr | Thr | Gln | Asp | Cys | Gln |  |      |
| 695        |            |            |            |            | 700        |            |     |     |     | 705 |     |     |     |     | 710 |  |      |
| ACG        | TAG        | AGCCATTCGT | CGACGACGCA | TTGACTTGAA | CTGCGGCTGT | TCCATATTTT |     |     |     |     |     |     |     |     |     |  | 1112 |
| Thr        | *          |            |            |            |            |            |     |     |     |     |     |     |     |     |     |  |      |
| ACCATATCAA | GTGCGCAGAT | CATGGATTCA | CGCACAGGGG | AGAACATCAC | TGCGCATCAG |            |     |     |     |     |     |     |     |     |     |  | 1172 |



GCACAGAATT C

1131

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met  Pro  Pro  Pro  Gln  Arg  Phe  Arg  Val  Gln  Ser  Lys  Asn  Tyr  Phe  Leu
 1              5              10              15

Thr  Tyr  Pro  Arg  Cys  Pro  Ile  Pro  Lys  Glu  Glu  Val  Leu  Ser  Gln  Leu
          20              25              30

Gln  Lys  Ile  His  Thr  Ala  Thr  Asn  Lys  Lys  Phe  Ile  Lys  Val  Cys  Glu
          35              40              45

Glu  Arg  His  Glu  Asn  Gly  Glu  Pro  His  Leu  His  Ala  Leu  Ile  Gln  Phe
          50              55              60

Glu  Gly  Lys  Phe  Val  Cys  Thr  Asn  Lys  Arg  Leu  Phe  Asp  Leu  Val  Ser
 65              70              75              80

Ser  Thr  Arg  Ser  Ala  Pro  Phe  His  Pro  Asn  Ile  Gln  Gly  Ala  Lys  Ser
          85              90              95

Ser  Ser  Asp  Val  Lys  Ala  Tyr  Ile  Asp  Lys  Asp  Gly  Val  Thr  Ile  Glu
          100             105             110

Trp  Gly  Gln  Phe  Gln  Val  Asp  Gly  Arg  Ser  Ala  Arg  Gly  Gly  Gln  Gln
          115             120             125

Ser  Ala  Asn  Asp  Ser  Tyr  Ala  Lys  Ala  Leu  Asn  Ala  Asp  Ser  Ile  Glu
          130             135             140

Ser  Ala  Leu  Thr  Ile  Leu  Lys  Glu  Glu  Gln  Pro  Lys  Asp  Tyr  Val  Leu
          145             150             155             160

Gln  His  His  Asn  Ile  Arg  Ser  Asn  Leu  Glu  Arg  Ile  Phe  Val  Lys  Val
          165             170             175

Pro  Glu  Pro  Trp  Val  Pro  Pro  Phe  Pro  Leu  Ser  Ser  Phe  Ile  Asn  Val
          180             185             190

Pro  Val  Val  Met  Gln  Glu  Trp  Val  Asp  Asp  Tyr  Phe  Gly  Arg  Gly  Ser
          195             200             205

Ala  Ala  Arg  Pro  Glu  Arg  Pro  Ile  Ser  Ile  Ile  Val  Glu  Gly  Asp  Ser
          210             215             220

Arg  Thr  Gly  Lys  Thr  Met  Trp  Ala  Arg  Ala  Leu  Gly  Pro  His  Asn  Tyr
          225             230             235             240

```

103

| 390               |                   |                   |                   | 395               |                   |                   |                   | 400               |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GAA<br>Glu        | CGT<br>Arg        | CAC<br>His<br>405 | SAG<br>Glu        | AAT<br>Asn        | GGT<br>Gly        | GAA<br>Glu        | CCT<br>Pro<br>410 | CAT<br>His        | CTT<br>Leu        | CAT<br>His        | GCG<br>Ala        | CTT<br>Leu<br>415 | ATT<br>Ile        | CAA<br>Gln        | TTC<br>Phe        | 192 |
| GAA<br>Glu        | GGT<br>Gly<br>420 | AAA<br>Lys        | TTC<br>Phe        | GTC<br>Val        | TGC<br>Cys        | ACA<br>Thr<br>425 | AAT<br>Asn        | AAA<br>Lys        | AGA<br>Arg        | TTG<br>Leu        | TTC<br>Phe<br>430 | GAC<br>Asp        | CTG<br>Leu        | GTA<br>Val        | TCC<br>Ser        | 240 |
| TCA<br>Ser<br>435 | ACC<br>Thr        | AGG<br>Arg        | TCA<br>Ser        | GCA<br>Ala        | CCT<br>Pro<br>440 | TTC<br>Phe        | CAT<br>His        | CCG<br>Pro        | AAC<br>Asn        | ATT<br>Ile<br>445 | CAG<br>Gln        | GGA<br>Gly        | GCT<br>Ala        | AAA<br>Lys        | TCA<br>Ser<br>450 | 288 |
| AGT<br>Ser        | TCA<br>Ser        | GAC<br>Asp        | GTC<br>Val        | AAG<br>Lys<br>455 | GCA<br>Ala        | TAC<br>Tyr        | ATC<br>Ile        | GAC<br>Asp        | AAA<br>Lys<br>460 | GAT<br>Asp        | GGA<br>Gly        | GTC<br>Val        | ACA<br>Thr        | ATC<br>Ile<br>465 | GAA<br>Glu        | 336 |
| TGG<br>Trp        | GGA<br>Gly        | CAA<br>Gln<br>470 | TTC<br>Phe        | CAA<br>Gln        | GTC<br>Val        | GAC<br>Asp        | GGC<br>Gly        | AGA<br>Arg<br>475 | TCT<br>Ser        | GCA<br>Ala        | AGA<br>Arg        | GGA<br>Gly        | GGT<br>Gly<br>480 | CAG<br>Gln        | CAG<br>Gln        | 384 |
| TCT<br>Ser        | GCC<br>Ala        | AAC<br>Asn<br>485 | GAC<br>Asp        | TCA<br>Ser        | TAT<br>Tyr        | GCA<br>Ala        | AAG<br>Lys<br>490 | GCA<br>Ala        | TTA<br>Leu        | AAC<br>Asn        | GCA<br>Ala        | GAT<br>Asp<br>495 | TCA<br>Ser        | ATT<br>Ile        | GAA<br>Glu        | 432 |
| TCT<br>Ser<br>500 | GCC<br>Ala        | TTG<br>Leu        | ACA<br>Thr        | ATA<br>Ile        | TTG<br>Leu        | AAG<br>Lys<br>505 | GAA<br>Glu        | GAA<br>Glu        | CAA<br>Gln        | CCG<br>Pro<br>510 | AAA<br>Lys        | GAT<br>Asp        | TAC<br>Tyr        | GTC<br>Val        | CTT<br>Leu        | 480 |
| TCA<br>Gln<br>515 | CAT<br>His        | CAC<br>His        | AAC<br>Asn        | ATC<br>Ile        | CGT<br>Arg<br>520 | TCT<br>Ser        | AAT<br>Asn        | CTC<br>Leu        | GAA<br>Glu        | CGG<br>Arg<br>525 | ATC<br>Ile        | TTC<br>Phe        | GTC<br>Val        | AAA<br>Lys        | GTG<br>Val<br>530 | 528 |
| CCG<br>Pro        | GAA<br>Glu        | CCA<br>Pro        | TGG<br>Trp        | GTT<br>Val<br>535 | CCT<br>Pro        | CCA<br>Pro        | TTT<br>Phe        | CCG<br>Pro        | TTG<br>Leu<br>540 | TCA<br>Ser        | TCA<br>Ser        | TTC<br>Phe        | CGC<br>Arg        | AAT<br>Asn<br>545 | GTT<br>Val        | 576 |
| CCG<br>Pro        | GTT<br>Val        | GTT<br>Val        | ATG<br>Met<br>550 | CAA<br>Gln        | GAA<br>Glu        | TGG<br>Trp        | GTT<br>Val        | GAC<br>Asp<br>555 | GAC<br>Asp        | TAT<br>Tyr        | TTC<br>Phe        | GGA<br>Gly        | AGG<br>Arg<br>560 | GGT<br>Gly        | TCC<br>Ser        | 624 |
| GCT<br>Ala        | GCG<br>Ala        | CGG<br>Arg<br>565 | CCG<br>Pro        | GAA<br>Glu        | AGA<br>Arg        | CCT<br>Pro<br>570 | ATT<br>Ile        | AGT<br>Ser        | ATC<br>Ile        | ATC<br>Ile        | GTC<br>Val        | GAA<br>Glu<br>575 | GGT<br>Gly        | GAT<br>Asp        | TCA<br>Ser        | 672 |
| CGA<br>Arg        | ACC<br>Thr<br>580 | GGA<br>Gly        | AAG<br>Lys        | ACA<br>Thr        | ATG<br>Met        | TGG<br>Trp<br>585 | GCT<br>Ala        | CGT<br>Arg        | GCA<br>Ala        | TTA<br>Leu        | GGA<br>Gly<br>590 | CCA<br>Pro        | CAT<br>His        | AAT<br>Asn        | TAT<br>Tyr        | 720 |
| TTG<br>Leu<br>595 | AGC<br>Ser        | GGT<br>Gly        | CAT<br>His        | TTG<br>Leu        | GAC<br>Asp<br>600 | TTT<br>Phe        | AAT<br>Asn        | TCA<br>Ser        | CGT<br>Arg        | GTC<br>Val<br>605 | TAT<br>Tyr        | TCC<br>Ser        | AAC<br>Asn        | GCA<br>Ala        | GTG<br>Val<br>610 | 768 |
| GAA<br>Glu        | TAC<br>Tyr        | AAC<br>Asn        | GTC<br>Val        | ATT<br>Ile<br>615 | GAT<br>Asp        | GAC<br>Asp        | ATA<br>Ile        | AGC<br>Ser        | CCC<br>Pro<br>620 | AAT<br>Asn        | TAT<br>Tyr        | TTG<br>Leu        | AAG<br>Lys        | TTA<br>Leu<br>625 | AAG<br>Lys        | 816 |
| CAC<br>His        | TGG<br>Trp        | AAA<br>Lys        | GAA<br>Glu        | CTA<br>Leu        | ATT<br>Ile        | GGG<br>Gly        | GCA<br>Ala        | CAA<br>Gln        | AAG<br>Lys        | GAC<br>Asp        | TGG<br>Trp        | CAA<br>Gln        | TCT<br>Ser        | AAC<br>Asn        | TGT<br>Cys        | 864 |

|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 630                                                               | 635 | 640 |      |
| AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG   |     |     | 912  |
| Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val   |     |     |      |
| 645                                                               | 650 | 655 |      |
| TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA   |     |     | 960  |
| Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys   |     |     |      |
| 660                                                               | 665 | 670 |      |
| GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC   |     |     | 1008 |
| Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe   |     |     |      |
| 675                                                               | 680 | 685 | 690  |
| GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA   |     |     | 1056 |
| Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln   |     |     |      |
| 695                                                               | 700 | 705 |      |
| ACG TAG AGCCATTCGT CGACGACGCA TTGACTTGAA CTGCGGCTGT TCCATATTTT    |     |     | 1112 |
| Thr *                                                             |     |     |      |
| ACCATATCAA GTGCGCAGAT CATGGATTCA CGCACAGGGG AGAACATCAC TGCGCATCAG |     |     | 1172 |
| GCAGAGAATT C                                                      |     |     | 1183 |

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15  
 Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu  
 20 25 30  
 Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu  
 35 40 45  
 Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe  
 50 55 60  
 Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser  
 65 70 75 80  
 Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu  
 100 105 110  
 Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu |     |     |
| 130                                                             | 135 | 140 |
| Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu |     |     |
| 145                                                             | 150 | 155 |
| Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val |     |     |
|                                                                 | 165 | 170 |
| Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Arg Asn Val |     |     |
|                                                                 | 180 | 185 |
| Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser |     |     |
|                                                                 | 195 | 200 |
| Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser |     |     |
|                                                                 | 210 | 215 |
| Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr |     |     |
| 225                                                             | 230 | 235 |
| Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val |     |     |
|                                                                 | 245 | 250 |
| Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys |     |     |
|                                                                 | 260 | 265 |
| His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys |     |     |
|                                                                 | 275 | 280 |
| Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val |     |     |
|                                                                 | 290 | 295 |
| Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys |     |     |
| 305                                                             | 310 | 315 |
| Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe |     |     |
|                                                                 | 325 | 330 |
| Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln |     |     |
|                                                                 | 340 | 345 |
|                                                                 |     | 350 |

Thr \*

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

- (iii) HYPOTHETICAL: NO

(v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: SHGA191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CATCATTCGG CAATGTTCCG GT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bean Golden Mosaic Geminivirus

(B) STRAIN: Type II

(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC | 48  |
| Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu |     |
| 355 360 365 370                                                 |     |
| ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT | 96  |
| Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu |     |
| 375 380 385                                                     |     |
| CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG | 144 |
| Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu |     |
| 390 395 400                                                     |     |
| GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC | 192 |
| Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe |     |
| 405 410 415                                                     |     |
| GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC | 240 |
| Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser |     |
| 420 425 430                                                     |     |
| TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA | 288 |
| Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser |     |
| 435 440 445 450                                                 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AGT | TCA | GAC | CTC | AAG | CCA | TAC | ATC | GAC | AAA | GAT | GGA | CTC | ACA | ATC | GAA | 335  |
| Ser | Ser | Asp | Val | Lys | Ala | Tyr | Ile | Asp | Lys | Asp | Gly | Val | Thr | Ile | Glu |      |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |     |      |
| TGG | GGA | CAA | TTC | CAA | GTC | GAC | GGC | AGA | TCT | GCA | AGA | GGA | GGT | CAG | CAG | 384  |
| Trp | Gly | Gln | Phe | Gln | Val | Asp | Gly | Arg | Ser | Ala | Arg | Gly | Gly | Gln | Gln |      |
|     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |     |     |      |
| TCT | GCC | AAC | GAC | TCA | TAT | GCA | AAG | GCA | TTA | AAC | GCA | GAT | TCA | ATT | GAA | 432  |
| Ser | Ala | Asn | Asp | Ser | Tyr | Ala | Lys | Ala | Leu | Asn | Ala | Asp | Ser | Ile | Glu |      |
|     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |     |      |
| TCT | GCC | TTG | ACA | ATA | TTG | AAG | GAA | GAA | CAA | CCG | AAA | GAT | TAC | GTC | CTT | 480  |
| Ser | Ala | Leu | Thr | Ile | Leu | Lys | Glu | Glu | Gln | Pro | Lys | Asp | Tyr | Val | Leu |      |
|     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |     |      |
| CAA | CAT | CAC | AAC | ATC | CGT | TCT | AAT | CTC | GAA | CGG | ATC | TTC | GTC | AAA | GTG | 528  |
| Gln | His | His | Asn | Ile | Arg | Ser | Asn | Leu | Glu | Arg | Ile | Phe | Val | Lys | Val |      |
| 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |     | 530 |      |
| CCG | GAA | CCA | TGG | GTT | CCT | CCA | TTT | CCG | TTG | TCA | TCA | TTC | ATC | AAT | GTT | 576  |
| Pro | Glu | Pro | Trp | Val | Pro | Pro | Phe | Pro | Leu | Ser | Ser | Phe | Ile | Asn | Val |      |
|     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     | 545 |     |      |
| CCG | GTT | GTT | ATG | CAA | GAA | TGG | GTT | GAC | GAC | TAT | TTC | GGA | AGG | GGT | TCC | 624  |
| Pro | Val | Val | Met | Gln | Glu | Trp | Val | Asp | Asp | Tyr | Phe | Gly | Arg | Gly | Ser |      |
|     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |     |     |      |
| GCT | GCG | CGG | CCG | GAA | AGA | CCT | ATT | AGT | ATC | ATC | GTC | AGA | GGT | GAT | TCA | 672  |
| Ala | Ala | Arg | Pro | Glu | Arg | Pro | Ile | Ser | Ile | Ile | Val | Arg | Gly | Asp | Ser |      |
|     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |     |     |      |
| CGA | ACC | GGA | AAG | ACA | ATG | TGG | GCT | CGT | GCA | TTA | GGA | CCA | CAT | AAT | TAT | 720  |
| Arg | Thr | Gly | Lys | Thr | Met | Trp | Ala | Arg | Ala | Leu | Gly | Pro | His | Asn | Tyr |      |
|     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |     |     |      |
| TTG | AGC | GGT | CAT | TTG | GAC | TTT | AAT | TCA | CGT | GTC | TAT | TCC | AAC | GCA | GTG | 768  |
| Leu | Ser | Gly | His | Leu | Asp | Phe | Asn | Ser | Arg | Val | Tyr | Ser | Asn | Ala | Val |      |
| 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |     | 610 |      |
| GAA | TAC | AAC | GTC | ATT | GAT | GAC | ATA | AGC | CCC | AAT | TAT | TTG | AAG | TTA | AAG | 816  |
| Glu | Tyr | Asn | Val | Ile | Asp | Asp | Ile | Ser | Pro | Asn | Tyr | Leu | Lys | Leu | Lys |      |
|     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     | 625 |     |      |
| CAC | TGG | AAA | GAA | CTA | ATT | GGG | GCA | CAA | AAG | GAC | TGG | CAA | TCT | AAC | TGT | 864  |
| His | Trp | Lys | Glu | Leu | Ile | Gly | Ala | Gln | Lys | Asp | Trp | Gln | Ser | Asn | Cys |      |
|     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |     |     |      |
| AAA | TAT | GGA | AAG | CCG | GTT | CAA | ATT | AAA | GGA | GGA | ATA | CCA | TCA | ATC | GTG | 912  |
| Lys | Tyr | Gly | Lys | Pro | Val | Gln | Ile | Lys | Gly | Gly | Ile | Pro | Ser | Ile | Val |      |
|     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |     |     |      |
| TTG | TGC | AAT | CCA | GGT | GAG | GGT | TCC | AGT | TAT | AAA | GAC | TTC | CTC | GAC | AAA | 960  |
| Leu | Cys | Asn | Pro | Gly | Glu | Gly | Ser | Ser | Tyr | Lys | Asp | Phe | Leu | Asp | Lys |      |
|     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |     |      |
| GAA | GAA | AAC | CGA | GCT | TTA | CAC | AAC | TGG | ACT | ATT | CAT | AAT | GCG | ATC | TTC | 1008 |
| Glu | Glu | Asn | Arg | Ala | Leu | His | Asn | Trp | Thr | Ile | His | Asn | Ala | Ile | Phe |      |
| 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     | 690 |      |

CTC ACC CTC ACA GCC CCE CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA  
 Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln  
 695 700 705

1036

ACG TAG  
 Thr \*

1062

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15  
 Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu  
 20 25 30  
 Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu  
 35 40 45  
 Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe  
 50 55 60  
 Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser  
 65 70 75 80  
 Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu  
 100 105 110  
 Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu  
 130 135 140  
 Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu  
 145 150 155 160  
 Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val  
 165 170 175  
 Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val  
 180 185 190  
 Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser  
 195 200 205



Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Arg Gly Asp Ser  
 210 215 220  
 Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr  
 225 230 235 240  
 Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val  
 245 250 255  
 Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys  
 260 265 270  
 His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys  
 275 280 285  
 Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val  
 290 295 300  
 Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys  
 305 310 315 320  
 Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe  
 325 330 335  
 Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln  
 340 345 350  
 Thr \*

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: SHGA221

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCATCGTCAG AGGTGATTCA C

21

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1062 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

= TOPOLOGY: Circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bean Golden Mosaic Geminivirus

(B) STRAIN: Type II

(C) INDIVIDUAL ISOLATE: Guatemala

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC | 48  |
| Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu |     |
| 355 360 365 370                                                 |     |
| ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT | 96  |
| Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu |     |
| 375 380 385                                                     |     |
| CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG | 144 |
| Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu |     |
| 390 395 400                                                     |     |
| GAA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC | 192 |
| Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe |     |
| 405 410 415                                                     |     |
| GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC | 240 |
| Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser |     |
| 420 425 430                                                     |     |
| TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA | 288 |
| Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser |     |
| 435 440 445 450                                                 |     |
| AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA | 336 |
| Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu |     |
| 455 460 465                                                     |     |
| TGG GGA CAA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG | 384 |
| Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln |     |
| 470 475 480                                                     |     |
| TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA | 432 |
| Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu |     |
| 485 490 495                                                     |     |
| TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT | 480 |
| Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu |     |
| 500 505 510                                                     |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG | 523  |
| Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val |      |
| 515 520 525 530                                                 |      |
| CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT | 575  |
| Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val |      |
| 535 540 545                                                     |      |
| CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC | 624  |
| Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser |      |
| 550 555 560                                                     |      |
| GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA | 672  |
| Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser |      |
| 565 570 575                                                     |      |
| CGA ACC GGA CAC ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT | 720  |
| Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr |      |
| 580 585 590                                                     |      |
| TTG AGC GGT CAT TTG GAC TTT AAT TCA CGT GTC TAT TCC AAC GCA GTG | 768  |
| Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val |      |
| 595 600 605 610                                                 |      |
| GAA TAC AAC GTC ATT GAT GAC ATA AGC CCC AAT TAT TTG AAG TTA AAG | 816  |
| Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys |      |
| 615 620 625                                                     |      |
| CAC TGG AAA GAA CTA ATT GGG GCA CAA AAG GAC TGG CAA TCT AAC TGT | 864  |
| His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys |      |
| 630 635 640                                                     |      |
| AAA TAT GGA AAG CCG GTT CAA ATT AAA GGA GGA ATA CCA TCA ATC GTG | 912  |
| Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val |      |
| 645 650 655                                                     |      |
| TTG TGC AAT CCA GGT GAG GGT TCC AGT TAT AAA GAC TTC CTC GAC AAA | 960  |
| Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys |      |
| 660 665 670                                                     |      |
| GAA GAA AAC CGA GCT TTA CAC AAC TGG ACT ATT CAT AAT GCG ATC TTC | 1008 |
| Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe |      |
| 675 680 685 690                                                 |      |
| GTC ACC CTC ACA GCC CCC CTC TAT CAA AGC ACA ACA CAG GAT TGC CAA | 1056 |
| Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln |      |
| 695 700 705                                                     |      |
| ACG TAG                                                         | 1062 |
| Thr *                                                           |      |

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15  
 Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu  
 20 25 30  
 Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu  
 35 40 45  
 Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe  
 50 55 60  
 Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser  
 65 70 75 80  
 Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu  
 100 105 110  
 Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu  
 130 135 140  
 Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu  
 145 150 155 160  
 Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val  
 165 170 175  
 Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val  
 180 185 190  
 Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser  
 195 200 205  
 Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser  
 210 215 220  
 Arg Thr Gly His Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr  
 225 230 235 240  
 Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val  
 245 250 255  
 Glu Tyr Asn Val Ile Asp Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys  
 260 265 270  
 His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys  
 275 280 285  
 Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val  
 290 295 300

Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys  
 305 310 315 320  
 Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe  
 325 330 335  
 Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln  
 340 345 350  
 Thr \*

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: SHGA228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAACCGGACA CACAATGTGG GC

22

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1062 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Bean Golden Mosaic Geminivirus
  - (B) STRAIN: Type II
  - (C) INDIVIDUAL ISOLATE: Guatemala
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1062

## X11 SEQUENCE DESCRIPTION: SEQ ID NO:54:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCA CCA CCT CAA AGA TTT AGA GTT CAG TCG AAA AAC TAT TTC CTC | 48  |
| Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu |     |
| 355 360 365 370                                                 |     |
| ACT TAT CCT CGT TGC CCT ATA CCG AAA GAA GAA GTT CTT TCG CAA CTT | 96  |
| Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu |     |
| 375 380 385                                                     |     |
| CAG AAG ATT CAT ACA GCC ACG AAT AAA AAA TTC ATC AAA GTC TGT GAG | 144 |
| Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu |     |
| 390 395 400                                                     |     |
| AA CGT CAC GAG AAT GGT GAA CCT CAT CTT CAT GCG CTT ATT CAA TTC  | 192 |
| Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe |     |
| 405 410 415                                                     |     |
| GAA GGT AAA TTC GTC TGC ACA AAT AAA AGA TTG TTC GAC CTG GTA TCC | 240 |
| Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser |     |
| 420 425 430                                                     |     |
| TCA ACC AGG TCA GCA CCT TTC CAT CCG AAC ATT CAG GGA GCT AAA TCA | 288 |
| Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser |     |
| 435 440 445 450                                                 |     |
| AGT TCA GAC GTC AAG GCA TAC ATC GAC AAA GAT GGA GTC ACA ATC GAA | 336 |
| Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu |     |
| 455 460 465                                                     |     |
| TGG GGA CCA TTC CAA GTC GAC GGC AGA TCT GCA AGA GGA GGT CAG CAG | 384 |
| Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln |     |
| 470 475 480                                                     |     |
| TCT GCC AAC GAC TCA TAT GCA AAG GCA TTA AAC GCA GAT TCA ATT GAA | 432 |
| Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu |     |
| 485 490 495                                                     |     |
| TCT GCC TTG ACA ATA TTG AAG GAA GAA CAA CCG AAA GAT TAC GTC CTT | 480 |
| Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu |     |
| 500 505 510                                                     |     |
| CAA CAT CAC AAC ATC CGT TCT AAT CTC GAA CGG ATC TTC GTC AAA GTG | 528 |
| Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val |     |
| 515 520 525 530                                                 |     |
| CCG GAA CCA TGG GTT CCT CCA TTT CCG TTG TCA TCA TTC ATC AAT GTT | 576 |
| Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val |     |
| 535 540 545                                                     |     |
| CCG GTT GTT ATG CAA GAA TGG GTT GAC GAC TAT TTC GGA AGG GGT TCC | 624 |
| Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser |     |
| 550 555 560                                                     |     |
| GCT GCG CGG CCG GAA AGA CCT ATT AGT ATC ATC GTC GAA GGT GAT TCA | 672 |
| Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser |     |
| 565 570 575                                                     |     |
| CGA ACC GGA AAG ACA ATG TGG GCT CGT GCA TTA GGA CCA CAT AAT TAT | 720 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Arg | Thr | Gly | Lys | Thr | Met | Tcp | Ala | Arg | Ala | Leu | Gly | Pro | His | Asn | Tyr |      |
| 530 |     |     |     |     |     | 595 |     |     |     |     | 590 |     |     |     |     |      |
| TTG | AGC | GGT | CAT | TTG | GAC | TTT | AAT | TCA | CGT | GTC | TAT | TCC | AAC | GCA | GTG | 753  |
| Leu | Ser | Gly | His | Leu | Asp | Phe | Asn | Ser | Arg | Val | Tyr | Ser | Asn | Ala | Val |      |
| 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |     | 610 |      |
| GAA | TAC | AAC | GTC | ATT | AGA | GAC | ATA | AGC | CCC | AAT | TAT | TTG | AAG | TTA | AAG | 815  |
| Glu | Tyr | Asn | Val | Ile | Arg | Asp | Ile | Ser | Pro | Asn | Tyr | Leu | Lys | Leu | Lys |      |
|     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     | 625 |     |      |
| CAC | TGG | AAA | GAA | CTA | ATT | GGG | GCA | CAA | AAG | GAC | TGG | CAA | TCT | AAC | TGT | 864  |
| His | Trp | Lys | Glu | Leu | Ile | Gly | Ala | Gln | Lys | Asp | Trp | Gln | Ser | Asn | Cys |      |
|     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |     |     |      |
| AAA | TAT | GGA | AAG | CCG | GTT | CAA | ATT | AAA | GGA | GGA | ATA | CCA | TCA | ATC | GTG | 912  |
| Lys | Tyr | Gly | Lys | Pro | Val | Gln | Ile | Lys | Gly | Gly | Ile | Pro | Ser | Ile | Val |      |
|     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |     |     |      |
| TTG | TGC | AAT | CCA | GGT | GAG | GGT | TCC | AGT | TAT | AAA | GAC | TTC | CTC | GAC | AAA | 960  |
| Leu | Cys | Asn | Pro | Gly | Glu | Gly | Ser | Ser | Tyr | Lys | Asp | Phe | Leu | Asp | Lys |      |
|     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |     |      |
| GAA | GAA | AAC | CGA | GCT | TTA | CAC | AAC | TGG | ACT | ATT | CAT | AAT | GCG | ATC | TTC | 1008 |
| Glu | Glu | Asn | Arg | Ala | Leu | His | Asn | Trp | Thr | Ile | His | Asn | Ala | Ile | Phe |      |
| 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     | 690 |      |
| GTC | ACC | CTC | ACA | GCC | CCC | CTC | TAT | CAA | AGC | ACA | ACA | CAG | GAT | TGC | CAA | 1056 |
| Val | Thr | Leu | Thr | Ala | Pro | Leu | Tyr | Gln | Ser | Thr | Thr | Gln | Asp | Cys | Gln |      |
|     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     | 705 |     |      |
| ACG | TAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1062 |
| Thr | *   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Pro Pro Pro Gln Arg Phe Arg Val Gln Ser Lys Asn Tyr Phe Leu  
 1 5 10 15  
 Thr Tyr Pro Arg Cys Pro Ile Pro Lys Glu Glu Val Leu Ser Gln Leu  
 20 25 30  
 Gln Lys Ile His Thr Ala Thr Asn Lys Lys Phe Ile Lys Val Cys Glu  
 35 40 45  
 Glu Arg His Glu Asn Gly Glu Pro His Leu His Ala Leu Ile Gln Phe  
 50 55 60  
 Glu Gly Lys Phe Val Cys Thr Asn Lys Arg Leu Phe Asp Leu Val Ser

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Ser Thr Arg Ser Ala Pro Phe His Pro Asn Ile Gln Gly Ala Lys Ser | 85  | 90  | 95  |
| Ser Ser Asp Val Lys Ala Tyr Ile Asp Lys Asp Gly Val Thr Ile Glu | 100 | 105 | 110 |
| Trp Gly Gln Phe Gln Val Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln | 115 | 120 | 125 |
| Ser Ala Asn Asp Ser Tyr Ala Lys Ala Leu Asn Ala Asp Ser Ile Glu | 130 | 135 | 140 |
| Ser Ala Leu Thr Ile Leu Lys Glu Glu Gln Pro Lys Asp Tyr Val Leu | 145 | 150 | 155 |
| Gln His His Asn Ile Arg Ser Asn Leu Glu Arg Ile Phe Val Lys Val | 165 | 170 | 175 |
| Pro Glu Pro Trp Val Pro Pro Phe Pro Leu Ser Ser Phe Ile Asn Val | 180 | 185 | 190 |
| Pro Val Val Met Gln Glu Trp Val Asp Asp Tyr Phe Gly Arg Gly Ser | 195 | 200 | 205 |
| Ala Ala Arg Pro Glu Arg Pro Ile Ser Ile Ile Val Glu Gly Asp Ser | 210 | 215 | 220 |
| Arg Thr Gly Lys Thr Met Trp Ala Arg Ala Leu Gly Pro His Asn Tyr | 225 | 230 | 235 |
| Leu Ser Gly His Leu Asp Phe Asn Ser Arg Val Tyr Ser Asn Ala Val | 245 | 250 | 255 |
| Glu Tyr Asn Val Ile Arg Asp Ile Ser Pro Asn Tyr Leu Lys Leu Lys | 260 | 265 | 270 |
| His Trp Lys Glu Leu Ile Gly Ala Gln Lys Asp Trp Gln Ser Asn Cys | 275 | 280 | 285 |
| Lys Tyr Gly Lys Pro Val Gln Ile Lys Gly Gly Ile Pro Ser Ile Val | 290 | 295 | 300 |
| Leu Cys Asn Pro Gly Glu Gly Ser Ser Tyr Lys Asp Phe Leu Asp Lys | 305 | 310 | 315 |
| Glu Glu Asn Arg Ala Leu His Asn Trp Thr Ile His Asn Ala Ile Phe | 325 | 330 | 335 |
| Val Thr Leu Thr Ala Pro Leu Tyr Gln Ser Thr Thr Gln Asp Cys Gln | 340 | 345 | 350 |
| Thr *                                                           |     |     |     |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotide Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: SHGA262

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACGTCATTAG AGACATAAGC

20

- (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Tomato-Infecting Geminivirus from Gautemala (TGV-GA1)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGATGAAGCT ATTGAAATGC TTCAAATCT GCCATGGTCA GTCGTCAAAC CAACGTACAT  | 60  |
| ACGAGTCGCC AGAGAGGAAC ACGCAGATGG ATTTCCGCAC CTCCACTGTC TCATCCAAC  | 120 |
| CTCCGGGAAG TCCAACATCA AGGATGCTAG ATTTTTCGAC CTCACTCACC CAGAAGGTCT | 180 |
| GCCAATTTTC ATCCAAAC                                               | 198 |

- (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## vi ORIGINAL SOURCE

(A) ORGANISM: Tomato-Infecting Geminivirus from Guatemala  
(TGV-GA1)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| AGGGTTCCGT GGCATTTTGG CAAATATGAG CCAGGACACC AGGGGGAGCT CTCTCTAAAA   | 60  |
| CTTTATTTTGG CTGGTGTCTT GGTGTCCCAT TTATACTAAA ACCCTCTTGG GGACACCAAG  | 120 |
| GGCAAATTTCG GCCATCCGCA ATAATATTAC CGGATGGCCG CGATTTTTTTT TGGACCTGGC | 180 |
| CCACTATCAG AAATTGCGTT GGGCCTTTCT GGATAAGTTA ACCAATCAAT ACACGTTTGG   | 240 |
| GTAGTCTAAT TATTACAACT TGGTCACCAA GTTGTTTTAT GGTCTATAAA TTTGTCGTTA   | 300 |
| TGTGTGTGGT CCAACCACGT AAATATTGAT AATGCCTAAG CGTGATGCCC CATGGCGCTT   | 360 |
| AATGGCGGGT ACCCTAAGG                                                | 379 |

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Tomato Leaf Curl Geminivirus from Southern  
India

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCGGATGGC CGCGATTTT TTTGTGGGCC CCTCAACGCA CTAAGTGACA AGGACATGCT  | 60  |
| AACCAATCAC ATGACGCGCT CAAAGCTTAA TTGTTTTGTG GTCCCCTATT TAACTTCGG  | 120 |
| CACCAAGTAT TGTATTTTGC ACTATGTGGG ATCCATTGTT AAACGAGTTT CCTGAAACCG | 180 |
| TTCACGGTTT TAGATGTATG TTAGCAGTTA AATATCTGCA ATTAGTAGAA AAGACCTATT | 240 |
| CTCCCGACAC ATTAGGTTAC GATTTAATTA GGGATTTAAT TTCAGTTATT AGGGCTAGAA | 300 |
| ATTATGTCGA AGCGACCAGC AGATATAATC ATTTCCACTC CCGCTTCGAA GGTACGTCGC | 360 |
| CGTCTCAACT TCGACAGCCC ATATGTGAGC CGTGCTGTG CCCCATTGT CCGCGTCACC   | 420 |
| AAAGCAAAAG CATGGGCGAA CAGGCCCATG AACAGAAAGC CCAGGATGTA CAGGATGTAC | 480 |
| AGAAGTCCAG ATGTCCCTAG AGGATGTGAA GGCCCATGTA AGGTCCAGTC GTTTGAGTCC | 540 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AGACACGATG TAGTCCATAT AGGCAAGGTC ATGTGTATTA GTGATGTAC TCSTGGAACC   | 510  |
| GGGCTGACCC ATAGAGTTGG TAAGCGTTTT TGTGTTAAGT CTGTTTACGT TTTGGGGAAG  | 550  |
| ATATGGATGG ACGAAAATAT AAAGACCAAG AATCATACGA ACAGTGTCTAT GTTTTTTCTT | 720  |
| GTTTCGTGACC GTCGTCTGTG TGACAAGCCA CAAGACTTTG GAGAGGTGTT CAATATGTTT | 780  |
| GACAACGAGC CTAGCACTGC TACTGTTAAG AATATGCACA GAGATCGTTA TCAGGTGTTG  | 840  |
| AGGAAGTGGC ATGCAACTGT CACCGGTGGA CAGTACGCTT CAAAGGAACA GGCATTAGTG  | 900  |
| AAGAAGTTTG TTAGGGTTAA TAATTATGTT GTTTATAACC AGCAAGAGGC TGGGAAATAT  | 960  |
| GAGAATCATA CTGAAAATGC ATTGATGTTG TATATGGCGT GTACTCACGC CTCTAACCTT  | 1020 |
| GTGTATGCTA CTTTGAAGAT ACGGATCTAT TTTTATGATT CAGTATCGAA TTAATAAATA  | 1080 |
| TTGAATTTTA TTGAATATGT TTGGTCTACA TATACAACGT GGTGTAATAC ATTCCATAAT  | 1140 |
| ACATAATCAA CGGCTCTGAT TACATTGTTA ATACTGATAA CTCCTAAATT ATTTAAGTAC  | 1200 |
| TTAAGCACTT GGGTCTTAAA TACCCTTAAG AAGCGACCAG TCGGAGGCTG TGAGGTCATC  | 1260 |
| CGGATTCGGT AGATTAGGAA ACATTTGTGT ATCCCCAACA CTTTCCTCAG GTTGTGATTG  | 1320 |
| AACTGTACTT GGTCCGTGAT GATGTCTTGG TTCATCAGGA ATGGCCGGTT GTGATGCTCT  | 1380 |
| GTTATCTTGA AATATAGGGG ATTTTGAATC TCCCAGATAA ACACGCCATT CTCTGCTTGA  | 1440 |
| GCTGCAGTGA TGAGTTCCCC TGTGCGTGAA TCCATGGTCG TGGCAGGCTA ATGCTATGAA  | 1500 |
| GTAAGAACAG CCGCACGGTA GATCAACTCG TCGACGTCTG GTCCCTTCTT TGGCTAGCCT  | 1560 |
| GTGCTGCACT TTGATTGGTA CCTGAGTAGA GTGGGCCTTC GAGGGTGACG AAGGTCGCAT  | 1620 |
| TCTTTATAGC CCAGAATTTT AGTTTAGAAT TCTTTCTTC ATCCAAGAAT TCTTTATAGC   | 1680 |
| TGGAGTTGGG TCCTGGATTG CAGAGGAAGA TTGTGGGAAT TCCGCCTTTA ATTTGAACTG  | 1740 |
| GCTTATTGTA CTTTCTATTT GATTGCCAGT CCCTTTGGGC CCCCATGAAT TCCTTAAAGT  | 1800 |
| GCTTTAGGTA GTTGGGGTCT ACGTCATCAA TTACGTTATA CCACGCATCA TTACTGTAGA  | 1860 |
| CCTTTGGGCT AAGGTCTAGA TGACCACACA AATAATTATG TGGTCCCAGT GATCTGGCCC  | 1920 |
| ACATAGTCTT GCCGGTCCTA CTGTCACCTT CAATCACTAT ACTTACGGGC CTCAAAGGCG  | 1980 |
| CGCACCTGAC GACGTTCTCG GCAGCCCACT CTTCAAGTTC ATCTGGAAC TGAATCAAAGG  | 2040 |
| AAGAAGAAGA AAAAGGAGAA GCATAAACCT CCATTGGAGG TGTAATAATC CTATCTAAAT  | 2100 |
| TACATTTTAA ATTATGATAT TGAAAAATAA AATCTTTAGG GAGTTTTTCC CTAATTATTG  | 2160 |
| CTAAAGCTGC TTCAGCTGAA CCTGCATTTA AGGCCTCTGC GGCAGCATCA TTAGCTGTCT  | 2220 |
| GTTGACCTCC TCGTGCAGAT CTTCCATCGA TCTGAAACTC ACCCCAGTCG ATGTAATCAC  | 2280 |
| TGTCCTTCTC GATGTAGGAC TTGACATCGG AGCTGAGCTT AGCTCCCTGG AAGTTTGGAT  | 2340 |

|                                                                                |      |
|--------------------------------------------------------------------------------|------|
| GGAAATTGGGT GGAGTTATTA GGGT <del>AG</del> TGA CATCGAAATG TCTGGGGTTT CGGAACCTGG | 2450 |
| ATTTACCCCTT GAATTGGATG AGGGCATGGA TATGCATAGA CCCATCTTGG TGTTCCTCTT             | 2460 |
| GGGCTACTCT GATAAATAAT TTATCAGATG GACAGAAAAT GTTTTAAAGG ATTTCGAGCA              | 2520 |
| TTTGTTCTTT GGGTATTGGG CATTTGGGAT AAGTAAGGAA GATATTTTTG GCATTAACAC              | 2580 |
| AAAAAGAGTT AATACGAGGC ATATTGAATT GGGGACACTC AAAACTCTGA GGAATGGGGG              | 2640 |
| ACTCGGGGGA CGCATTTATA AGGCGTCCCT AAATGGCATT TTTGTAATTT GGGAAAGTAA              | 2700 |
| TTCAAAATCC TCACGCTCCA AAAAGCGGCC ATCCGTATAA TATT                               | 2744 |

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato-Infecting Geminivirus from Mexico (Chino-like sympts)

## (ix) FEATURE:

- (A) NAME/KEY: unsure
- (B) LOCATION: 1220..1403

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAGGTGGTC CGATATATCC TGGGCTTGGT GTACATGGGC CTGTTAATTT AACGAGCGGC | 60  |
| CTTATCGAAT TTAGGGCCCA TACCCGTGCC ACGTGAATAA TTAGCAGGCG GGAAACCTTG | 120 |
| GAGGTCCCCG CCATTAAACG CCATGGGGCA TCCCGCTTGG CCATTTTGAA TTAAAGATAT | 180 |
| AAATGCACAT GCACGTGCAT TTATAGGACC ACACCTTGGT CACCAAGGCA CAAATATCTA | 240 |
| GACTTGACAG CCGGGATGTG ATTGGTCAGT CAAAATCAAA TAATTGGTGG TCCCATCTCT | 300 |
| TTATCTCTTT AATCTCAGCC CTCTATTCTG AGTGGTCCCC CAGATACTCC AAAAATCGC  | 360 |
| GGCCATCCGG TAATATTATA GGATGGCCGC TTTGCCCCCT GGAGTTCCCC CTGTGTGTTC | 420 |
| TAGTATTTAA GGGACTCCAG GACTCCAGAA ACATAGTACG GTTTTATGAG GCACTCTCCT | 480 |
| GGAGTCCTAC ACCATATTTG CGAAAATGCC ACTACCCCCA AAGTCATTTT GTTTACAATG | 540 |
| TAAAAACATT TTCTTAACAT ATCCACAATG CGATATCCCA AAGGATGAAG CTCTCGAAAT | 600 |
| GCTGCAGTCG TAAAAAATGG TCTGTCGTAA AACCCATATA CATAAGGGTA TCACGGGAGG | 660 |
| AGCATTCCGA TGGGTTTCCG CACTTGCACT GTCTCATCCA GCTAACTGGA AAGTGCAACA | 720 |

```

TCAAAGATGC TCGGTTCTTC GACATTACTC ACCCCCGGAG ATCTGECAG TTTCATCAA 730
ACGTTTCAGGC GGCTAAAGAC ACAAATGCCG TAAAGAATTA TATCACTAAA GATGGCGATT 840
ATTGCGAATC TGGAAAGTAC AAAGTTTCCG GGGGTTCCAA AGCAAATAAA GACGACGTCT 900
ACCATAACGC TGTAATGCA GCAAGTGCGA CAGAGGCGCT CGACATTATA AGGCTGGAGA 960
TCCAAGAACG TTCATTGTCA GCTATCATAA CGTTAAGTCT AACATCGAGC GCCTGTTCAA 1020
ACCTCCTCCT AAACCATGGA CTCCTCCTTA TCCAATTTCC TCGTTTAATA ACGTTCCTGA 1080
GGATATGCAA ACTTGGGTTG CTGAATATCT TGGTCGGACT TCCGCTGCGC GGCCAGATAG 1140
ACCGATTAGT ATTGTCATTG AGGGCGATTG GCGAAGGCAA GACAATGTGG GCACGTGCAT 1200
TAGGCCCCACA TAATTATTTG AGTGTACCT TGATTTCAT TCAAAAGTCT ATTCAAACGA 1260
TGTGGAGTAT AACGTCATTG ATGATATCAC GCCCATTATC TAAAGTTGAA ACCTGGAAAG 1320
AGCTTATTGG GGCCCAAAGG GACTGGCAGT CCAACTGTAA ATCGGAAACC AGTTCAAATT 1380
AACGCCGGGA TTCCATCAAT TGT 1403

```

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato-Infecting Geminivirus similar to Pepper Hausteco
- (C) INDIVIDUAL ISOLATE: Sinaloa, Mexico

## (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Torres-Pacheco, I  
Garzon-Tiznado,  
Herrera-Estrella, L  
Rivera-Bustmante, R
- (B) TITLE: Sequence from a new tomato-infecting  
geminivirus from Sinaloa, Mexico with some  
similarity to Pepper Hausteco Virus
- (C) JOURNAL: J. General Virology
- (D) VOLUME: 74
- (F) PAGES: 2225-2231
- (G) DATE: 1993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

CCCTGAATGT TCGGATGGAA ATGTGCTGAT CTGGTTGAGG ATACGAGGTC AAAGAATCTG 60

```

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TIGTTCGTGC ATTGGTATTT TCCTTCGAAC TGAATAAGCA CGTGCAGATG AGGTTGCCCA | 120 |
| TCCTCATGAG ATTCTTTGCA AATTTTGATG TACTTCTTGT TTACCGGCGT CGAGAGGTTT | 130 |
| TGTAGTTGAG CGAGAGCCTC TTCTTTGGAA ATGGAACATT GGGGATAGGT GAGGAAATAA | 240 |
| TTCTTGGCAT TTAAACGAAA TCGTTTAGGT AATGGCATAT TTGTAATAAG AGAGGTGTAC | 300 |
| ACCGATTGGA GCTCTTTAAC CTGAGCTTAT TGTATCGGTG TATTGGTAGC CAATATATAG | 360 |
| TATATGGGAG TTATCTAGGA TCTTCGTACA CGTGGAGGCC ATCCGTTATA ATATTACCGG | 420 |
| ATGGCCGACC GCTTACCTTA TCTATCCGTA CAGCTTTATT TTGAATTAAA GATGTTACTT | 480 |
| TTATGCTATC CAATGAGCGT GCGTCTGGA AGCTTAGTTA ACCGTTCCAG ACGTGGGGAC  | 540 |
| CAAGTAGTGT ATGACCACTT TATTGACTGT CAGCTTTATA AATTCAAATT AACACATAAG | 600 |
| TGGTCCATAT ACCTTTAATT CAAAATGCCT AAGCGTGATG CTCCTTGGCG ATTAACGGCG | 660 |
| GGGACCGCAA GATTAGCCGA ACTGGCAATA ATTCACGGGC TCTTATCATG GGCCCGAGTA | 720 |
| CTAGCAGGGC CTCAGCTTGG GTTAATCGCC CAATGTACAG GAAGCCCCGC ATTTATCGTA | 780 |

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato-Infecting Geminivirus similar to  
Pepper Hausteco
- (C) INDIVIDUAL ISOLATE: Sinaloa, Mexico

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTTATATTC AAAAGATATT TGGATTTTAA TATTAGCAAT TACAAATAAG CAATTTAATA | 60  |
| TGTATTCCAC TAGGTTTAGA CGTGGGTTAT CGTATGGTCC ACGTCGTTCT AATGCACGTA | 120 |
| ATTATGGTTT TAAACGCACA TTGGCCGTTA AGCGTTTTGA TGGTAATCGG CGCCAGAAGC | 180 |
| AAGTGAAGAA AACCGATGAA GAGTTAAAAA TGTCATCGCA GCGTATGCAT GAAAATCAGT | 240 |
| ATGGTCCAGA TTTTGTAATG GCGCATAACA CATCAATATC TACGTTTCATC AATTTCCAC | 300 |
| AAATGTGTAA GACTCAGCCC AATCGTAGCA GGTCCTATAT TAAGTTAAAA TGTTTGCATT | 360 |
| TTAAGGGAAC CGTTAAGATT GAACGTGTTG GGCTGAGTT AAATATGGCC GGGTTAAGTC  | 420 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CAAAGATTGA GGGAGTTTTG ACCGTGGTTG TTGTTGTTGA CCGTAAGCCG CATTTGAGTC | 480  |
| CCACTGGCAA CTTGCACACA TTTGATGAGT TATTTGGTGC AAGAATTCAT AGTCATGGTA | 540  |
| ACTTAGCTGT TACCCCTTCG TTGAAGGAAC GGTTCACAT TCGTCATGTG TTGAAGAGAG  | 600  |
| TTATCTCCGT TGAGAAGGAC ACTATGATGC TGGATCTAGA AGGATCCACG TGCCTGTCTA | 660  |
| ATCGGCGTTT TAATTGTTGG TCCACATTTA AGGACCTGGA TCCTTCATCA TGTAACGGCG | 720  |
| TCTATGACAA TATAAGTAAA AACGCCTTGT TAGTTTATTA TTGCTGGATG TCGGATGCTA | 780  |
| TGTCTAAGGC ATCCACATTT GTATCATTG ATTGGACTA TGTTGGTTGA GAAATAATAA   | 840  |
| ACTTGCGCAC TTTGCTCAAA TCTTTATTTT GTCACAAAAT AATATATTTA TTTCAACGAC | 900  |
| TTAGGCTGTG TCGGATTACA ATTACTGTTA ATACATTCAT GGACCGTAGT CTTCAAGTT  | 960  |
| CATTTAATTG GGCCAAGGAC ATAGTTATAT TTGAGTGGGT TCGTGTTAGA CCAACTTGTG | 1020 |
| ATGCTGAATC ACCTGGGTCT AGAACACTTC CGCCTAACTG ATGAAGATCT TTATACGGAT | 1080 |
| GTAATGCGCT ATGTCCTTGG GAGTCGGGAT TTGTGTGAGT GGTGCTATG GTGCTTCTAC  | 1140 |
| ATGCCCATGA TTCACCCGGT TTTAATTCAA TTGGGCCTGT AATGCCGAAC CTTGACATTG | 1200 |
| ATGCTGACCT CAATGG                                                 | 1216 |

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tomato-Infecting Geminivirus similar to  
Pepper Hausteco
- (C) INDIVIDUAL ISOLATE: Sinoloa, Mexico

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAATATCTAA CGTTTCAGGG GTGGTAGAGG ACGCTCCACG TCATTACACA TTTCTCCATG | 60  |
| TATGGACCAC ACTTTAATTT GAAATGAAGG CGCGCGATTG AACTCATCCA ACGACCCACA | 120 |
| TGATGCCACG TACACATAAC TCATAGTGCG CGCCAGCTGT ACCAAAGGAA AGAGAGTGG  | 180 |
| AGCGGTCGGC CATCCGGTAA TATTATAACG GATGGCCTCC ACGTGACGA AGATCCTAGA  | 240 |
| TAACTCCCAT ATACTATATA TTGGCTACCA ATACACCGAT ACCATCAGCA CAGGTTAAAG | 300 |
| AGCTCCAATC GGTGTACACC CTTCTTATTT CATAAATGCC ATTGCAATAT TTCTCTCTCT | 360 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAAACCAGCT GCCAATTCTA TATAACGCAG CTGCATGTTT ATTAAATTAA TCATACTAAT | 420  |
| TCTCTCTTCT CTCTCTTCTT CAGACGCTCT TGCTTGCTTC CTCACCGGTT TCTTCATAAA | 480  |
| TTCTTCATAG AATAGCAATA TCTTAACATC GAAGTAAGCT TATTTTTTGA ACTCTTTCAG | 540  |
| CAAATAATAA TTTGTCATTT TCGTTACCAT TATCATTGTT AGGTATAGCT TCTTATTGGC | 600  |
| AGCTTCATAC TCGGTAAGCC TTCAGCTGCG CAGCCAATTT TTCATATATG GATTCTAGGT | 660  |
| TGGCGAATCC TCCTAGTGCC TTCAATTATA TAGAATCCCA TAGAGATGAA TATCAGCTCT | 720  |
| CTCATGACTT AACTGAAATA GTACTTCAAT TTCCGTCAAC GGCCTCACAG TACGCAGCCA | 780  |
| GACTTAGTCG TAGCTGTATG AAAATTGACC ATTGCGTTAT CGAGTATAGA CAGCAGGTTC | 840  |
| CGATAAACGC AACTGGATCG GTAATAGTGG AAATCCATGA CAAGAGAATG ACTGACAATG | 900  |
| AATCATTACA AGCTTCCTGG ACATTTCCAC TAAGATGCAA CATTGATCTC CATTACTTCT | 960  |
| CGGCGTCCTT CTTCTCCTTG AAGGACCCCA TACCATGGAA GCTATATTAC CGGGTCTCAG | 1020 |
| ATACTAACGT ACATCAGAAC ACACATTTTG CCAAGTTCAA AGGCAAATTG AAGTTGTCCA | 1080 |
| CAGCTAAACA CTCTGTGGAT ATACCCTTCA                                  | 1110 |



## WE CLAIM:

1. A transgenic plant comprising chromosomal DNA, the plant harboring geminivirus DNA integrated into the chromosomal DNA, the geminivirus DNA encoding a protein required for geminivirus replication, and the geminivirus DNA conferring resistance to viral infection.
2. Transgenic plants according to claim 1 in which the geminivirus DNA is wild type DNA.
3. The transgenic plant according to claim 1 in which the geminivirus DNA comprises an ORF selected from the group consisting of AC1 and C1.
4. The transgenic plant according to claim 3 in which the geminivirus DNA comprises DNA encoding an amino acid sequence selected from the group consisting of FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGkt; and NviDDi.
5. The transgenic plant according to claim 1 in which the geminivirus DNA is a transdominant interference mutant of a geminivirus gene.
6. The transgenic plant according to claim 5 in which the geminivirus DNA comprises an ORF selected from the group consisting of AC1 and C1.
7. The transgenic plant according to claim 5 in which the geminivirus DNA encodes a sequence motif selected from the group consisting of a DNA-nicking domain and a NTP-binding domain.

8. The transgenic plant according to claim 7 in which at least one mutation region of the transdominant interference mutant of the geminivirus DNA encodes an amino acid sequence comprising FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGkt; and NviDDi.

9. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGkt; and NviDDi in the AC1 ORF.

10. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGkt; and NviDDi.

11. A transgenic plant according to claim 8 in which the geminivirus DNA is a ToMoV AC1 mutant selected from the group consisting of Sequence ID Nos. 3, 5, 7, 13, 14 and 15.

12. A transgenic plant according to claim 8 in which the geminivirus DNA is a TYLCV C1 mutant selected from the group consisting of Sequence ID Nos. 23, 26, and 29.

13. A transgenic plant according to claim 8 in which the geminivirus DNA is a BGMV AC1 mutant selected from the group consisting of Sequence ID Nos. 45, 48, 51, and 54.

14. A method of interfering with geminivirus infection of a transgenic plant comprising:

selecting a transgenic plant according to claim 1;  
and  
growing said transgenic plant.

1/1

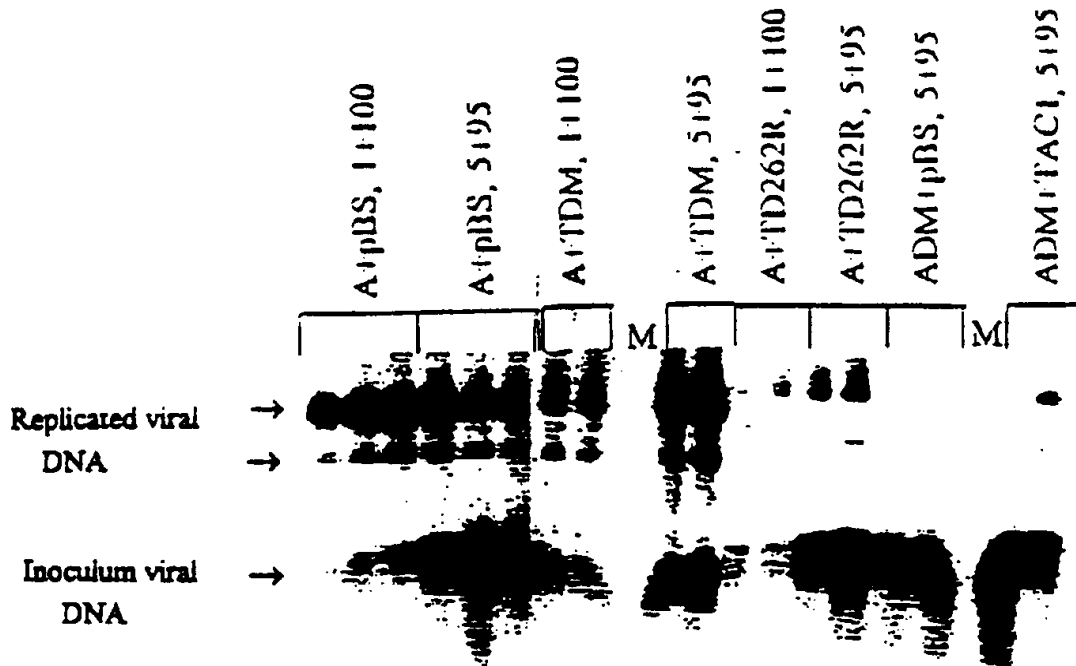


Fig. 1

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/06300

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 5/14, 7/04

US CL : 435/236; 800/205

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/172.3, 236, 320.1; 800/205

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN, MEDLINE, BIOSIS, EMBASE, WPIDS

search terms: geminivirus, tomato mottle virus, ToMoV, tomato yellow leaf curl virus, TYLCV, transgenic, C1, AC1, motif

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category*         | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                    | Relevant to claim No.            |
|-------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|
| X<br>--<br>Y      | KUNIK et al. Transgenic tomato plants expressing the tomato yellow leaf curl virus capsid protein are resistant to the virus. Bio/Technology. May 1994, Vol. 12, pages 500-504, see entire document.                  | 1-2, 14<br>-----<br>3-13         |
| Y                 | HANSON et al. Mutational analysis of a putative NTP-binding domain in the replication-associated protein (AC1) of bean golden mosaic geminivirus. Virology. 01 August 1995, Vol. 211, pages 1-9, see entire document. | 3-13                             |
| X,P<br>---<br>Y,P | NORIS et al. Resistance to tomato yellow curl geminivirus in Nicotiana benthamiana plants transformed with a truncated viral C1 gene. Virology. 01 October 1996, Vol. 224, pages 130-138, see entire document.        | 1-3, 5-6, 14<br>-----<br>4, 7-13 |

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

|                                          |     |                                                                                                                                                                                                                                              |
|------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| * Special categories of cited documents: | * T | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention                                              |
| * A                                      |     | document defining the general state of the art which is not considered to be of particular relevance                                                                                                                                         |
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| * L                                      |     | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)                                                                          |
| * O                                      |     | document referring to an oral disclosure, use, exhibition or other means                                                                                                                                                                     |
| * P                                      |     | document published prior to the international filing date but later than the priority date claimed                                                                                                                                           |
|                                          | * X | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone                                                                     |
|                                          | * Y | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
|                                          | * A | document member of the same patent family                                                                                                                                                                                                    |

Date of the actual completion of the international search

17 MAY 1997

Date of mailing of the international search report

1 JUL 1997

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

AMY NELSON

Telephone No. (703) 308-0196

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/06300

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                         | Relevant to claim No. |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| Y,P       | BENDAHDANE et al. Engineering resistance against tomato yellow curl virus (TYLCV) using antisense RNA. Plant Molecular Biology. January 1997, Vol. 33, pages 351-357, see entire document. | 1-14                  |
| X         | Database WPIL on Questel, week 9618. Derwent Publications Ltd. AN 96-179947. WO 9608573 (GRONENBORN, B.) 15                                                                                | 1-2, 14               |
| Y         | September 1995.                                                                                                                                                                            | 3-13                  |

- 127 -

8. The transgenic plant according to claim 7 in which at least one mutation region of the transdominant interference mutant of the geminivirus DNA encodes an amino acid sequence comprising FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGKt; and NviDDi.

9. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGKt; and NviDDi in the AC1 ORF.

10. The transgenic plant according to claims 7 or 8 in which the geminivirus DNA consists of at least one mutation of FLTYpxC; pHLHvliQ; vKxYxdKd; FHPNlQxak; EGx<sub>2</sub>RTGKt; and NviDDi.

11. A transgenic plant according to claim 8 in which the geminivirus DNA is a ToMoV AC1 mutant selected from the group consisting of Sequence ID Nos. 3, 5, 7, 13, 14 and 15.

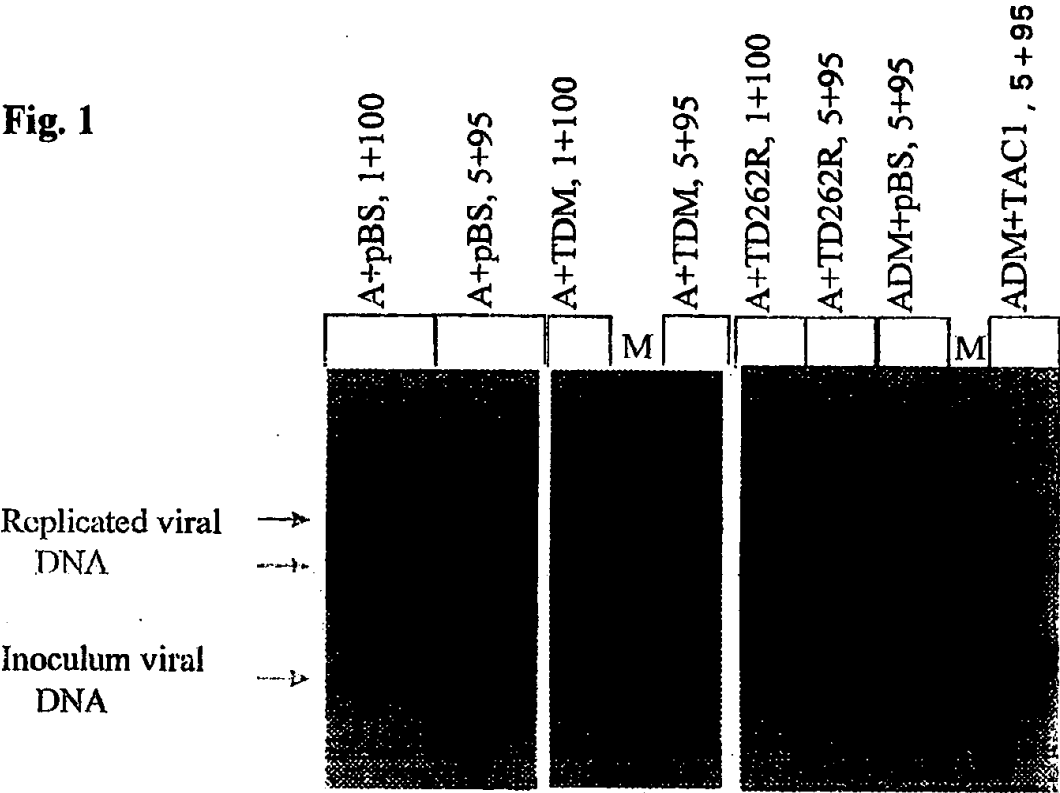
12. A transgenic plant according to claim 8 in which the geminivirus DNA is a TYLCV C1 mutant selected from the group consisting of Sequence ID Nos. 23, 26, and 29.

13. A transgenic plant according to claim 8 in which the geminivirus DNA is a BGMV AC1 mutant selected from the group consisting of Sequence ID Nos. 45, 48, 51, and 54.

14. A method of interfering with geminivirus infection of a transgenic plant comprising:

selecting a transgenic plant according to claim 1;  
and  
growing said transgenic plant.

Fig. 1



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/06300

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 5/14, 7/04

US CL :435/236; 800/205

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/172.3, 236, 320.1; 800/205

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN, MEDLINE, BIOSIS, EMBASE, WPIDS

search terms: geminivirus, tomato mottel virus, ToMöV, tomato yellow leaf curl virus, TYLCV, transgenic, C1, AC1, motif

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                    | Relevant to claim No. |
|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| X         | KUNIK et al. Transgenic tomato plants expressing the tomato yellow leaf curl virus capsid protein are resistant to the virus. Bio/Technology. May 1994, Vol. 12, pages 500-504, see entire document.                  | 1-2, 14               |
| Y         |                                                                                                                                                                                                                       | 3-13                  |
| Y         | HANSON et al. Mutational analysis of a putative NTP-binding domain in the replication-associated protein (AC1) of bean golden mosaic geminivirus. Virology. 01 August 1995, Vol. 211, pages 1-9, see entire document. | 3-13                  |
| X,P       | NORIS et al. Resistance to tomato yellow curl geminivirus in Nicotiana benthamiana plants transformed with a truncated viral C1 gene. Virology. 01 October 1996, Vol. 224, pages 130-138, see entire document.        | 1-3, 5-6, 14          |
| Y,P       |                                                                                                                                                                                                                       | 4, 7-13               |

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

|                                          |     |                                                                                                                                                                                                                                              |
|------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| * Special categories of cited documents: | * T | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principles or theory underlying the invention                                             |
| * A                                      |     | document defining the general state of the art which is not considered to be of particular relevance                                                                                                                                         |
| * E                                      |     | earlier document published on or after the international filing date                                                                                                                                                                         |
| * L                                      |     | document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)                                                                           |
| * O                                      |     | document referring to an oral disclosure, use, exhibition or other means                                                                                                                                                                     |
| * P                                      |     | document published prior to the international filing date but later than the priority date claimed                                                                                                                                           |
|                                          | * X | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone                                                                     |
|                                          | * Y | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
|                                          | * A | document member of the same patent family                                                                                                                                                                                                    |

Date of the actual completion of the international search

17 MAY 1997

Date of mailing of the international search report

11 JUL 1997

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

AMY NELSON

Telephone No. (703) 308-0196



**INTERNATIONAL SEARCH REPORT**

L. national application No.

PCT/US97/06300

**C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category* | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                         | Relevant to claim No. |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| Y,P       | BENDAHDANE et al. Engineering resistance against tomato yellow curl virus (TYLCV) using antisense RNA. Plant Molecular Biology. January 1997, Vol. 33, pages 351-357, see entire document. | 1-14                  |
| X<br>Y    | Database WPIL on Questel, week 9618. Derwent Publications Ltd. AN 96-179947. WO 9608573 (GRONENBORN, B.) 15 September 1995.                                                                | 1-2, 14<br>3-13       |